

Db 115 MHPPLPQVHDVTKMPLPFYEVYVGLIRPTTLASTSSQRFEEAHFTFALTPOQVQILIT 174
Qy 121 SREVLPGAKCDYTIQVQLRFLCETSCQEDYFPPNLFVKNVGLKCLPLPGYLPPTKNGAE 180
Db 175 SREVLPGAKCDYTIQVQLRFLCETSCQEDYFPPNLFVKNVGLKCLPLPGYLPPTKNGAE 234
Qy 181 PKRPSRPINITPLARLSATVPNTIIVNWSSEFGNYSLSVYLVRQLTAGTLLQKLRAGI 240
Db 235 PKRPSRPINITPLARLSATVPNTIIVNWSSEFGNYSLSVYLVRQLTAGTLLQKLRAGI 294
Qy 241 RNPDSRALIKEKLTADPDSEVATTSLRVSLMCPGLGKRLTVPCRALTCALHQSFDAAALY 300
Db 295 RNPDSRALIKEKLTADPDSEVATTSLRVSLMCPGLGKRLTVPCRALTCALHQSFDAAALY 354
Qy 301 LQWNEKPTWTCPCVCDKAPYESLIIDGLFMEILNCSDCDEIQFMDGSCWCPMKPKKEA 360
Db 355 LQWNEKPTWTCPCVCDKAPYESLIIDGLFMEILNCSDCDEIQFMDGSCWCPMKPKKEA 414
Qy 361 SEVCPPPGYGLDGLQYSPVQGGDPSENKKVVEIDLTIESSSDEEDLPPTKKHCVTSAA 420
Db 415 SEVCPPPGYGLDGLQYSPVQGGDPSENKKVVEIDLTIESSSDEEDLPPTKKHCVTSAA 474
Qy 421 IPALPGSKGALTSQHQPSSVLRSPAMGTGLGDFLSSLPHEYPAPPLGADIQGLDLFSF 480
Db 475 IPALPGSKGALTSQHQPSSVLRSPAMGTGLGDFLSSLPHEYPAPPLGADIQGLDLFSF 534
Qy 481 LQTESQHYSPVITSLDEQDTHGFFOFRGTTPPHFLGPLAPTGLSSHRSATPAPAGRVS 540
Db 535 LQTESQHYSPVITSLDEQDTHGFFOFRGTTPPHFLGPLAPTGLSSHRSATPAPAGRVS 594
Qy 541 SIVAPGSLREGHGGPLPSGSLTGCRSDVITSLD 574
Db 595 SIVAPGALRECHGGPLPSGSLTGCRSDIISLD 628

RESULT 6

US-09-836-941-2
; Sequence 2, Application US/09836941
; Patent No. 6465200
; GENERAL INFORMATION:
; APPLICANT: Kase, Matthew, R.
; APPLICANT: Baughn, Mariah, R.
; TITLE OF INVENTION: TRANSCRIPTION FACTOR REGULATORY PROTEIN
; FILE REFERENCE: PC-0001 US
; CURRENT APPLICATION NUMBER: US/09/836,941
; CURRENT FILING DATE: 2001-04-17
; PRIOR APPLICATION NUMBER: 09/286,132
; PRIOR FILING DATE: 1999-04-01
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PERL Program
; SEQ ID NO 2
; LENGTH: 628
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: 2667068
US-09-836-941-2

Query Match 96.7%; Score 2944; DB 4; Length 628;
Best Local Similarity 96.3%; Pred. No. 7.5e-266;
Matches 553; Conservative 7; Mismatches 14; Indels 0; Gaps 0;
Qy 1 MKIKELRRRFPRTKLGPSDLISLPPGTSPVGSPLASIPPTLLTPGTLGPKREVD 60
Db 55 MKIKELRRRFPRTKLGPSDLISLPPGTSPVGSPLASIPPTLLTPGTLGPKREVD 114
Qy 61 MHPPLPQVHDVTKMPLPFYEVYVGLIRPTTLASTSSQRFEEAHFTFALTPOQVQILIT 120
Db 115 MHPPLPQVHDVTKMPLPFYEVYVGLIRPTTLASTSSQRFEEAHFTFALTPOQVQILIT 174
Qy 121 SREVLPGAKCDYTIQVQLRFLCETSCQEDYFPPNLFVKNVGLKCLPLPGYLPPTKNGAE 180

Db 175 SREVLPGAKCDYTIQVQLRFLCETSCQEDYFPPNLFVKNVGLKCLPLPGYLPPTKNGAE 234
Qy 181 PKRPSRPINITPLARLSATVPNTIIVNWSSEFGNYSLSVYLVRQLTAGTLLQKLRAGI 240
Db 235 PKRPSRPINITPLARLSATVPNTIIVNWSSEFGNYSLSVYLVRQLTAGTLLQKLRAGI 294
Qy 241 RNPDSRALIKEKLTADPDSEVATTSLRVSLMCPGLGKRLTVPCRALTCALHQSFDAAALY 300
Db 295 RNPDSRALIKEKLTADPDSEVATTSLRVSLMCPGLGKRLTVPCRALTCALHQSFDAAALY 354
Qy 301 LQWNEKPTWTCPCVCDKAPYESLIIDGLFMEILNCSDCDEIQFMDGSCWCPMKPKKEA 360
Db 355 LQWNEKPTWTCPCVCDKAPYESLIIDGLFMEILNCSDCDEIQFMDGSCWCPMKPKKEA 414
Qy 361 SEVCPPPGYGLDGLQYSPVQGGDPSENKKVVEIDLTIESSSDEEDLPPTKKHCVTSAA 420
Db 415 SEVCPPPGYGLDGLQYSPVQGGDPSENKKVVEIDLTIESSSDEEDLPPTKKHCVTSAA 474
Qy 421 IPALPGSKGALTSQHQPSSVLRSPAMGTGLGDFLSSLPHEYPAPPLGADIQGLDLFSF 480
Db 475 IPALPGSKGALTSQHQPSSVLRSPAMGTGLGDFLSSLPHEYPAPPLGADIQGLDLFSF 534
Qy 481 LQTESQHYSPVITSLDEQDTHGFFOFRGTTPPHFLGPLAPTGLSSHRSATPAPAGRVS 540
Db 535 LQTESQHYSPVITSLDEQDTHGFFOFRGTTPPHFLGPLAPTGLSSHRSATPAPAGRVS 594
Qy 541 SIVAPGSLREGHGGPLPSGSLTGCRSDVITSLD 574
Db 595 SIVAPGALRECHGGPLPSGSLTGCRSDIISLD 628

RESULT 7

US-09-062-440-6
; Sequence 6, Application US/09062440
; Patent No. 6207422
; GENERAL INFORMATION:
; APPLICANT: Brown, Arthur M.
; APPLICANT: Yang, Qing
; APPLICANT: Wible, Barbara A.
; TITLE OF INVENTION: A Protein that Enhances Expression of
; TITLE OF INVENTION: Potassium Channels on Cell Surfaces
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Callage, Halter & Griswold LLP
; STREET: 1400 McDonald Investment Center, 800 Superior
; CITY: Cleveland
; STATE: Ohio
; COUNTRY: US
; ZIP: 44114
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/062,440
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Docherty, Pamela A.
; REGISTRATION NUMBER: 40591
; REFERENCE/DOCKET NUMBER: 22884/04004
; TELEPHONE: 2162228200
; TELEFAX: 2162410816
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 574 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide

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Query Match	100.0%;	Score 3056;	DB 4;	Length 628;
Best Local Similarity	100.0%;	Pred. No. 2.2e-272;		
Matches 574; Conservative	0;	Mismatches 0;	Indels 0;	Gaps 0;
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Ddb	55	MKIKELYRRFRPKTIGPSDLSLLSPGPTSPVSGPGLAPIPPTLLAPGTLLGPCKREVD	114	
OY	61	MHPPLPQPVPHPVTMKLPDFEYVGELIRPTTLASTSSORFEAHFFALTTPQOVQOILT	120	
Ddb	115	MHPPLPQPVPHPVTMKLPDFEYVGELIRPTTLASTSSORFEAHFFALTTPQOVQOILT	174	
OY	121	SREVLPGAKCDYTIQVLRFCLCETSCPDEDYPNNLFVKVNGKLCPLPGYLPTTKNGAE	180	
Ddb	175	SREVLPGAKCDYTIQVLRFCLCETSCPDEDYPNNLFVKVNGKLCPLPGYLPTTKNGAE	234	
OY	181	PKRPSRPINITPLARLSATVPNTIVNWSSEFGNYSLSVYLVRQLTAGTLLQKLRAKGI	240	
Ddb	235	PKRPSRPINITPLARLSATVPNTIVNWSSEFGNYSLSVYLVRQLTAGTLLQKLRAKGI	294	
OY	241	RNPDSRALIKEKLTADDPSEVAATTSLRVSLMCPLGKMRITVPCRALTCAGHQSFDAALY	300	
Ddb	295	RNPDSRALIKEKLTADDPSEVAATTSLRVSLMCPLGKMRITVPCRALTCAGHQSFDAALY	354	

	Query Match	96.3%	Score 2944;	DB 3;	Length 574;
	Best Local Similarity	96.3%;	Pred. No. 3.9e-262;		
	Matches 553; Conservative	7;	Mismatches 14;	Indels 0;	Gaps 0;
QY	1	MKIKELYRRRFRKTLGPSDLSLLSLPCTSVGSPGPIAPPTTLALPGLTGLPKRREVD	60		
ddb	1	MKIKELYRRRFRKTLGPSDLSLLSLPCTSVGSPGPIAPPTTLTGTTLGPKRREVD	60		
QY	61	MHPPLQVPHVDVTKPLPFYEVYVYGLIRPPTTLASTSSORFEEAHFTFALTPOOVCOILT	120		


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; CURRENT APPLICATION NUMBER: US/09/286,132
; CURRENT FILING DATE: 1999-04-01
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PERL Program
; SEQ ID NO 2
; LENGTH: 628
; TYPE: PRP
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: 2667068
US-09-286-132-2

Query Match      100.0%   Score 544; DB 3; Length 628;
Best Local Similarity 100.0%; Pred. No. 2.3e-54;
Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TWTCPVCDKKAPYBSLIIDGLFMELSSCDSDCIQFMEDGSCWCPMKPKKEASEVCPPPG 60
DQ 363 TWTCPVCDKKAPYBSLIIDGLFMELSSCDSDCIQFMEDGSCWCPMKPKKEASEVCPPPG 422
QY 61 YGLDGLQYSPVGGDPSENKKKVEVIDLTIESSSDEEDL 99
DQ 423 YGLDGLQYSPVGGDPSENKKKVEVIDLTIESSSDEEDL 461

RESULT 6
US-09-836-941-2
; Sequence 2, Application US/09836941
; Patent No. 6465200.
; GENERAL INFORMATION:
; APPLICANT: Kaser, Matthew, R.
; APPLICANT: Baughn, Mariah, R.
; TITLE OF INVENTION: TRANSCRIPTION FACTOR REGULATORY PROTEIN
; FILE REFERENCE: PC-0001 US
; CURRENT APPLICATION NUMBER: US/09/836,941
; CURRENT FILING DATE: 2001-04-17
; PRIOR APPLICATION NUMBER: 09/286,132
; PRIOR FILING DATE: 1999-04-01
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PERL Program
; SEQ ID NO 2
; LENGTH: 628
; TYPE: PRP
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: 2667068
US-09-836-941-2

Query Match      100.0%   Score 544; DB 4; Length 628;
Best Local Similarity 100.0%; Pred. No. 2.3e-54;
Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TWTCPVCDKKAPYBSLIIDGLFMELSSCDSDCIQFMEDGSCWCPMKPKKEASEVCPPPG 60
DQ 363 TWTCPVCDKKAPYBSLIIDGLFMELSSCDSDCIQFMEDGSCWCPMKPKKEASEVCPPPG 422
QY 61 YGLDGLQYSPVGGDPSENKKKVEVIDLTIESSSDEEDL 99
DQ 423 YGLDGLQYSPVGGDPSENKKKVEVIDLTIESSSDEEDL 461

RESULT 7
US-09-062-440-6
; Sequence 6, Application US/09062440
; Patent No. 6207422
; GENERAL INFORMATION:
; APPLICANT: Brown, Arthur M.
; APPLICANT: Yang, Qing
; APPLICANT: Wible, Barbara A.
; TITLE OF INVENTION: A Protein that Enhances Expression of
; TITLE OF INVENTION: Potassium Channels on Cell Surfaces
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESS: Calfee, Halter & Griswold LLP
; STREET: 1400 McDonald Investment Center, 800 Superior
; STREET: Avenue
; CITY: Cleveland
; STATE: Ohio
; COUNTRY: US
; ZIP: 44114
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/062,440
; FILING DATA:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Doherly, Pamela A.
; REGISTRATION NUMBER: 40591
; REFERENCE/DOCKET NUMBER: 22884/04004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 2166224200
; TELEFAX: 2162410816
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 574 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 37..38
; OTHER INFORMATION: /note= "glycine or serine"
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 41..42
; OTHER INFORMATION: /note= "proline or serine"
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 48..49
; OTHER INFORMATION: /note= "alanine or threonine"
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 115..116
; OTHER INFORMATION: /note= "valine or leucine"
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 335..336
; OTHER INFORMATION: /note= "serine or asparagine"
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 381..382
; OTHER INFORMATION: /note= "glycine or glutamic acid"
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 383..384
; OTHER INFORMATION: /note= "aspartic acid or
; OTHER INFORMATION: asparagine"
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; OTHER INFORMATION: /note= "isoproline or glutamine"
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; NAME/KEY: Peptide
; LOCATION: 390..391
; OTHER INFORMATION: /note= "lysine or arginine"
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 416..417
; OTHER INFORMATION: /note= "serine or proline"
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NAME/KEY: Peptide
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OTHER INFORMATION: /note= "valine or alanine"
FEATURE:
NAME/KEY: Peptide
LOCATION: 451..452
OTHER INFORMATION: /note= "glycine or serine"
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NAME/KEY: Peptide
LOCATION: 489..490
OTHER INFORMATION: /note= "glycine or serine"
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NAME/KEY: Peptide
LOCATION: 501..502
OTHER INFORMATION: /note= "alanine or threonine"
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NAME/KEY: Peptide
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OTHER INFORMATION: /note= "tyrosine or phenylalanine"
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LOCATION: 513..514
OTHER INFORMATION: /note= "serine or proline"
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NAME/KEY: Peptide
LOCATION: 528..529
OTHER INFORMATION: /note= "cysteine or arginine"
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NAME/KEY: Peptide
LOCATION: 535..536
OTHER INFORMATION: /note= "proline or alanine"
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NAME/KEY: Peptide
LOCATION: 547..548
OTHER INFORMATION: /note= "glycine or serine"
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NAME/KEY: Peptide
LOCATION: 548..549
OTHER INFORMATION: /note= "alanine or serine"
FEATURE:
NAME/KEY: Peptide
LOCATION: 570..571
OTHER INFORMATION: /note= "isoleucine or valine"
US-09-062-440-6

Query Match 95.6%; Score 520; DB 3; Length 574;
Best Local Similarity 96.0%; Pred. No. 1.2e-51;
Matches 95; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 TWTCPVCDKAPYSLIIDGLFMELSSCSDCDEIQFMEDGSCWCPMKPKKEASEVCPPPG 60
DB 309 TWTCPVCDKAPYSLIIDGLFMELSSCSDCDEIQFMEDGSCWCPMKPKKEASEVCPPPG 368
QY 61 YGLDGLQYSPVQGGPSENKKKVEVIDLTIESSSDEEDL 99
DB 369 YGLDGLQYSPVQGGPSENKKKVEVIDLTIESSSDEEDL 407

RESULT 8
US-09-062-440-7
Sequence 7, Application US/09062440
Patent No. 6207422

GENERAL INFORMATION:
APPLICANT: Brown, Arthur M.
APPLICANT: Yang, Qing
TITLE OF INVENTION: A Protein that Enhances Expression of
TITLE OF INVENTION: Potassium Channels on Cell Surfaces
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESS: Calfee, Halter & Griswold LLP
STREET: 1400 McDonald Investment Center, 800 Superior

STREET: Avenue
CITY: Cleveland
STATE: Ohio
COUNTRY: US
ZIP: 44114
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/062.440
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Docherty, Pamela A.
REGISTRATION NUMBER: 40591
REFERENCE/DOCKET NUMBER: 22884.04004
TELECOMMUNICATION INFORMATION:
TELEPHONE: 2166228200
TELEFAX: 2162410816
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 99 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-09-062-440-7

Query Match 95.0%; Score 517; DB 3; Length 99;
Best Local Similarity 94.9%; Pred. No. 2.8e-52;
Matches 94; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 TWTCPVCDKAPYSLIIDGLFMELSSCSDCDEIQFMEDGSCWCPMKPKKEASEVCPPPG 60
DB 1 TWTCPVCDKAPYSLIIDGLFMELSSCSDCDEIQFMEDGSCWCPMKPKKEASEVCPPPG 60
QY 61 YGLDGLQYSPVQGGPSENKKKVEVIDLTIESSSDEEDL 99
DB 61 YGLDGLQYSPVQGGPSENKKKVEVIDLTIESSSDEEDL 99

RESULT 9
US-09-742-495-7
Sequence 7, Application US/09712495
Patent No. 6391561

GENERAL INFORMATION:
APPLICANT: Brown, Arthur
APPLICANT: Wible, Barbara
APPLICANT: Yang, Qing
TITLE OF INVENTION: Protein That Enhances Expression of Potassium Channels on Cell Surfaces
TITLE OF INVENTION: and Nucleic Acids That Encode The Same
FILE REFERENCE: 22884.04046
CURRENT APPLICATION NUMBER: US/09/712.495
CURRENT FILING DATE: 2000-11-14
PRIOR APPLICATION NUMBER: 09/062.440
PRIOR FILING DATE: 1998-04-17
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PatentIn version 3.0
SEQ ID NO 7
LENGTH: 99
TYPE: PRT
ORGANISM: Homo sapiens
US-09-712-495-7

Query Match 95.0%; Score 517; DB 4; Length 99;
Best Local Similarity 94.9%; Pred. No. 2.8e-52;
Matches 94; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 TWTCPVCDKAPYSLIIDGLFMELSSCSDCDEIQFMEDGSCWCPMKPKKEASEVCPPPG 60

QY 61 MHPPLPOVHPDVTMKLPFVYVYVGLIRPTTTLASTSSQRFEEAHFTFALTPOOQOILT 120
DB 78 -----PVHPDVTMKLPFVYVYVGLIRPTTTLASTSSQRFEEAHFTFALTPOOQOILT 130
QY 121 SREVLPQAKLDYTIQVLRFLCETSLPQEDYPPNLFVKNVGNKLCPLPGYLPPTKNGAE 180
DB 131 SREVLPQAKLDYTIQVLRFLCETSLPQEDYPPNLFVKNVGNKLCPLPGYLPPTKNGAE 190
QY 181 PKRP-----SRPINITPKARLSATVPNTIIVNWSSEFGRTNLSVLYVRQLTAG 229
DB 191 PRGPAVRSTSHPLWDSQPLSPFP-----SLIGHLSLDG--ITPCPCLVRQLTAG 238
QY 230 TLQKLRAGIRPNDRHSRALIKGLTADPDGVAATTSRLVSLMCPGLKMLTTPCRALTC 289
DB 239 TLQKLRAGIRPNDRHSRALIKGLTADPDGVAATTSRLVSLMCPGLKMLTTPCRALTC 298
QY 290 AHLQSFSAALYLQWNE-KPTWTCPCVCDKAPKAPESLIIDGLFMEILXSCSDCDEIQFMEDG 348
DB 299 AHLQSFDAALYLQWNEKPTWTCPCVCDKAPKAPESLIIDGLFMEILXSCSDCDEIQFMEDG 358
QY 349 STCPMPKKEASEVCPGPGGLDGLQYSPVQXGKPSVLRSPAMGTGLXDFLSLPLHVEYPPAPPLG 408
DB 359 SWCPMPKKEASEVCPGPGGLDGLQYSAVQEGIQPESKKRVEVIDLTIESSSDEEDLPP 418
QY 409 TKKHCVTSAAIPALPGSKGLTSGHOPSSVLRSPAMGTGLXDFLSLPLHVEYPPAPPLG 468
DB 419 TKKHCVTSAAIPALPGSKGLTSGHOPSSVLRSPAMGTGLXDFLSLPLHVEYPPAPPLG 478
QY 469 ADIQGLDLFSLQTES-QYXPSVITSLDEQDLXGHFFQXRFTHXFLGPLAPTLGSSSHXS 527
DB 479 ADIQGLDLFSLQTES-QYXPSVITSLDEQDLXGHFFQXRFTHXFLGPLAPTLGSSSHXS 538
QY 528 ATPAPXGRVSSIVAPGXLRREGHGGPLPSGSLTGCSDIXSLD 572
DB 539 STAPPXGRVSSIVAPGXLRREGHGGPLPSGSLTGCSDIXSLD 583

RESULT 10

US-09-836-941-17
; Sequence 17, Application US/09836941
; Patent No. 6465200
; GENERAL INFORMATION:
; APPLICANT: Kaser, Matthew, R.
; TITLE OF INVENTION: TRANSCRIPTION FACTOR REGULATORY PROTEIN
; FILE REFERENCE: PC-0001 US
; CURRENT APPLICATION NUMBER: US/09/836,941
; CURRENT FILING DATE: 2001-04-17
; PRIOR APPLICATION NUMBER: 09/286,132
; PRIOR FILING DATE: 1999-04-01
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PERL Program
; SEQ ID NO 17
; LENGTH: 583
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; OTHER INFORMATION: 92689028
US-09-836-941-17

Query Match 78.7%; Score 2317; DB 4; Length 583;
Best Local Similarity 79.0%; Pred. No. 1.5e-221;
Matches 462; Conservative 14; Mismatches 49; Indels 60; Gaps 6;
QY 1 MKIKELVRRFRPKTLGSDLSLSPGTSVPGSPXPLAXIPPTLLXPGTLGPKREV 60
DB 46 MKIKELVRRFRPKTLGSDLSLSPGTSVPGSPXPLAXIPPTLLXPGTLGPKREV 77
QY 61 MHPPLPOVHPDVTMKLPFVYVYVGLIRPTTTLASTSSQRFEEAHFTFALTPOOQOILT 120
DB 78 -----PVHPDVTMKLPFVYVYVGLIRPTTTLASTSSQRFEEAHFTFALTPOOQOILT 130
QY 121 SREVLPQAKLDYTIQVLRFLCETSLPQEDYPPNLFVKNVGNKLCPLPGYLPPTKNGAE 180

DB 131 SREVLPQAKLDYTIQVLRFLCETSLPQEDYPPNLFVKNVGNKLCPLPGYLPPTKNGAE 190
QY 181 PKRP-----SRPINITPKARLSATVPNTIIVNWSSEFGRTNLSVLYVRQLTAG 229
DB 191 PRGPAVRSTSHPLWDSQPLSPFP-----SLIGHLSLDG--ITPCPCLVRQLTAG 238
QY 230 TLQKLRAGIRPNDRHSRALIKGLTADPDGVAATTSRLVSLMCPGLKMLTTPCRALTC 289
DB 239 TLQKLRAGIRPNDRHSRALIKGLTADPDGVAATTSRLVSLMCPGLKMLTTPCRALTC 298
QY 290 AHLQSFSAALYLQWNE-KPTWTCPCVCDKAPKAPESLIIDGLFMEILXSCSDCDEIQFMEDG 348
DB 299 AHLQSFDAALYLQWNEKPTWTCPCVCDKAPKAPESLIIDGLFMEILXSCSDCDEIQFMEDG 358
QY 349 STCPMPKKEASEVCPGPGGLDGLQYSPVQXGKPSVLRSPAMGTGLXDFLSLPLHVEYPPAPPLG 408
DB 359 SWCPMPKKEASEVCPGPGGLDGLQYSAVQEGIQPESKKRVEVIDLTIESSSDEEDLPP 418
QY 409 TKKHCVTSAAIPALPGSKGLTSGHOPSSVLRSPAMGTGLXDFLSLPLHVEYPPAPPLG 468
DB 419 TKKHCVTSAAIPALPGSKGLTSGHOPSSVLRSPAMGTGLXDFLSLPLHVEYPPAPPLG 478
QY 469 ADIQGLDLFSLQTES-QYXPSVITSLDEQDLXGHFFQXRFTHXFLGPLAPTLGSSSHXS 527
DB 479 ADIQGLDLFSLQTES-QYXPSVITSLDEQDLXGHFFQXRFTHXFLGPLAPTLGSSSHXS 538
QY 528 ATPAPXGRVSSIVAPGXLRREGHGGPLPSGSLTGCSDIXSLD 572
DB 539 STAPPXGRVSSIVAPGXLRREGHGGPLPSGSLTGCSDIXSLD 583

RESULT 11

US-08-399-696-102
; Sequence 102, Application US/08399696
; Patent No. 5756669
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: p53-BINDING POLYPEPTIDES AND
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING SAME
; NUMBER OF SEQUENCES: 126
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/399,696
; FILING DATE: 02-MAR-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/156,671
; FILING DATE: 22-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 15522-000710
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 102:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 597 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-399-696-102

Query Match 50.3%; Score 1480.5; DB 1; Length 597;
Best Local Similarity 53.1%; Pred. No. 2.3e-138;
Matches 326; Conservative 77; Mismatches 152; Indels 59; Gaps 19;

1 CURRENT FILING DATE: 2001-04-17
2 PRIOR APPLICATION NUMBER: 09/286,132
3 PRIOR FILING DATE: 1999-04-01
4 NUMBER OF SEQ ID NOS: 17
5 SOFTWARE: PERL Program
6 SEQ ID NO 17
7 LENGTH: 583
8 TYPE: PRT
9 ORGANISM: Mus musculus
10 FEATURE: -
11 OTHER INFORMATION: G2689028
12 US-09-836-941-17

Query Match 95.0%; Score 516; DB 4; Length 583;
Best Local Similarity 96.0%; Pred. No. 1.1e-52;
Matches 95; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
Qy 1 TWTCPCVCDKKAPYESLIIDGLFMEILNSCSDCDIQLFMEIDGSCWCPMKPKKEASEVCPPPG 60
Db 318 TWTCPCVCDKKAPYESLIIDGLFMEILNSCSDCDIQLFMEIDGSCWCPMKPKKEASEVCPPPG 377
Qy 61 YGLDGLQYSPVOENQSENKRVVEIDLTIESSSDEEDL 99
Db 378 YGLDGLQYSAVQEGIQESKRVVEIDLTIESSSDEEDL 416

RESULT 13

US-09-062-440-6
Sequence 6, Application US/09062440
Patent No. 6207422
GENERAL INFORMATION:
APPLICANT: Brown, Arthur M.
APPLICANT: Yang, Qing
APPLICANT: Noble, Barbara A.
TITLE OF INVENTION: A Protein that Enhances Expression of
TITLE OF INVENTION: Potassium Channels on Cell Surfaces
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Calfee, Halter & Griswold LLP
STREET: 1400 McDonald Investment Center, 800 Superior
STREET: Avenue
CITY: Cleveland
STATE: Ohio
COUNTRY: US
ZIP: 44114
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA: US/09/062,440
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Docherty, Pamela A.
REGISTRATION NUMBER: 40591
REFERENCE/DOCKET NUMBER: 22884/04004
TELECOMMUNICATION INFORMATION:
TELEPHONE: 2166228200
TELEFAX: 2162410816
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 574 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE:
NAME/KEY: Peptide
LOCATION: 37..38

OTHER INFORMATION: /note= "glycine or serine"
FEATURE:
NAME/KEY: Peptide
LOCATION: 41..42
OTHER INFORMATION: /note= "proline or serine"
FEATURE:
NAME/KEY: Peptide
LOCATION: 48..49
OTHER INFORMATION: /note= "alanine or threonine"
FEATURE:
NAME/KEY: Peptide
LOCATION: 115..116
OTHER INFORMATION: /note= "valine or leucine"
FEATURE:
NAME/KEY: Peptide
LOCATION: 335..336
OTHER INFORMATION: /note= "serine or asparagine"
FEATURE:
NAME/KEY: Peptide
LOCATION: 381..382
OTHER INFORMATION: /note= "glycine or glutamic acid"
FEATURE:
NAME/KEY: Peptide
LOCATION: 383..384
OTHER INFORMATION: /note= "aspartic acid or
asparagine"
FEATURE:
NAME/KEY: Peptide
LOCATION: 384..385
OTHER INFORMATION: /note= "isoproline or glutamine"
FEATURE:
NAME/KEY: Peptide
LOCATION: 390..391
OTHER INFORMATION: /note= "lysine or arginine"
FEATURE:
NAME/KEY: Peptide
LOCATION: 416..417
OTHER INFORMATION: /note= "serine or proline"
FEATURE:
NAME/KEY: Peptide
LOCATION: 431..432
OTHER INFORMATION: /note= "valine or alanine"
FEATURE:
NAME/KEY: Peptide
LOCATION: 451..452
OTHER INFORMATION: /note= "glycine or serine"
FEATURE:
NAME/KEY: Peptide
LOCATION: 489..490
OTHER INFORMATION: /note= "glycine or serine"
FEATURE:
NAME/KEY: Peptide
LOCATION: 501..502
OTHER INFORMATION: /note= "alanine or threonine"
FEATURE:
NAME/KEY: Peptide
LOCATION: 508..509
OTHER INFORMATION: /note= "tyrosine or phenylalanine"
FEATURE:
NAME/KEY: Peptide
LOCATION: 513..514
OTHER INFORMATION: /note= "serine or proline"
FEATURE:
NAME/KEY: Peptide
LOCATION: 528..529
OTHER INFORMATION: /note= "cysteine or arginine"
FEATURE:
NAME/KEY: Peptide
LOCATION: 535..536
OTHER INFORMATION: /note= "proline or alanine"
FEATURE:
NAME/KEY: Peptide
LOCATION: 547..548

OTHER INFORMATION: /note= "glycine or serine"
FEATURE:
NAME/KEY: Peptide
LOCATION: 548..549
OTHER INFORMATION: /note= "alanine or serine"
FEATURE:
NAME/KEY: Peptide
LOCATION: 570..571
OTHER INFORMATION: /note= "isoleucine or valine"
US-09-062-440-6

Query Match 94.1%; Score 511; DB 3; Length 574;
Best Local Similarity 94.9%; Pred. No. 4.3e-52;
Matches 94; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 1 WTCPVCDKKAPYESLIIDGLFMEILNCSDCDEIQFMEDGSCWCPMKPKKEASEVCPPPG 60
DB 309 WTCPVCDKKAPYESLIIDGLFMEILNCSDCDEIQFMEDGSCWCPMKPKKEASEVCPPPG 368
QY 61 YLDGLQYSPVOGQSGNSKKEVEVIDLTIESSSDEEDL 99
DB 369 YLDGLQYSPVOGQSGNSKKEVEVIDLTIESSSDEEDL 407

RESULT 14
US-09-062-440-10
Sequence 10, Application US/09062440
Patent No. 6207422
GENERAL INFORMATION:
APPLICANT: Brown, Arthur M.
APPLICANT: Yang, Qing
APPLICANT: Wible, Barbara A.
TITLE OF INVENTION: A Protein that Enhances Expression of
TITLE OF INVENTION: Potassium Channels on Cell Surfaces
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESS: Calfee, Halter & Griswold LLP
STREET: 1400 McDonald Investment Center, 800 Superior
CITY: Cleveland
STATE: Ohio
COUNTRY: US
ZIP: 44114
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/062,440
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Docherty, Pamela A.
REGISTRATION NUMBER: 40591
REFERENCE/DOCKET NUMBER: 22884/04004
TELECOMMUNICATION INFORMATION:
TELEPHONE: 2166228200
TELEFAX: 2162410816
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 98 amino acids
TYPE: amino acid
STRANDEDNESS: not-relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Peptide
LOCATION: 25..26
OTHER INFORMATION: /note= "serine or asparagine"
FEATURE:
NAME/KEY: Peptide
LOCATION: 61..62

OTHER INFORMATION: /note= "glycine or glutamic acid"
FEATURE:
NAME/KEY: Peptide
LOCATION: 63..64
OTHER INFORMATION: /note= "aspartic acid or asparagine"
FEATURE:
NAME/KEY: Peptide
LOCATION: 64..65
OTHER INFORMATION: /note= "proline or glutamine"
FEATURE:
NAME/KEY: Peptide
LOCATION: 70..71
OTHER INFORMATION: /note= "lysine or arginine"
US-09-062-440-10

Query Match 93.2%; Score 506; DB 3; Length 98;
Best Local Similarity 94.9%; Pred. No. 1.6e-52;
Matches 93; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 2 WTCPCVCDKKAPYESLIIDGLFMEILNCSDCDEIQFMEDGSCWCPMKPKKEASEVCPPPG 61
DB 1 WTCPCVCDKKAPYESLIIDGLFMEILNCSDCDEIQFMEDGSCWCPMKPKKEASEVCPPPG 60
QY 62 GLDGLQYSPVOGQSGNSKKEVEVIDLTIESSSDEEDL 99
DB 61 GLDGLQYSPVOGQSGNSKKEVEVIDLTIESSSDEEDL 98

RESULT 15
US-09-712-495-10
Sequence 10, Application US/09712495
Patent No. 6391561
GENERAL INFORMATION:
APPLICANT: Brown, Arthur
APPLICANT: Wible, Barbara
APPLICANT: Yang, Qing
TITLE OF INVENTION: Protein That Enhances Expression of Potassium Channels on Cell
TITLE OF INVENTION: and Nucleic Acids That Encode The Same
FILE REFERENCE: 22884/04046
CURRENT APPLICATION NUMBER: US/09/712,495
CURRENT FILING DATE: 2000-11-14
PRIOR APPLICATION NUMBER: 09/062,440
PRIOR FILING DATE: 1998-04-17
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patent in version 3.0
SEQ ID NO 10
LENGTH: 98
TYPE: PRT
FEATURE:
ORGANISM: synthetic construct
NAME/KEY: misc_feature
LOCATION: (25)..(25)
OTHER INFORMATION: Xaa = serine-or asparagine
NAME/KEY: misc_feature
LOCATION: (61)..(61)
OTHER INFORMATION: Xaa = glycine or glutamic acid
NAME/KEY: misc_feature
LOCATION: (63)..(63)
OTHER INFORMATION: Xaa = aspartic acid or asparagine
NAME/KEY: misc_feature
LOCATION: (64)..(64)
OTHER INFORMATION: Xaa = proline or glutamine
US-09-712-495-10

Query Match 91.3%; Score 496; DB 4; Length 98;
Best Local Similarity 93.9%; Pred. No. 2.5e-51;
Matches 92; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 2 WTCPCVCDKKAPYESLIIDGLFMEILNCSDCDEIQFMEDGSCWCPMKPKKEASEVCPPPG 61
DB 1 WTCPCVCDKKAPYESLIIDGLFMEILNCSDCDEIQFMEDGSCWCPMKPKKEASEVCPPPG 60

Db 370 GLDGLQSPVQGGPSENKKKVEIDLTISSDEEDL 407

RESULT 5
US-09-712-495-4
; Sequence 4, Application US/09712495
; Patent No. 6391561
; GENERAL INFORMATION:
; APPLICANT: Brown, Arthur
; APPLICANT: Wible, Barbara
; APPLICANT: Yang, Qing
; TITLE OF INVENTION: Protein That Enhances Expression of Potassium Channels on Cell Surfaces
; TITLE OF INVENTION: and Nucleic Acids That Encode The Same
; FILE REFERENCE: 22884/04046
; CURRENT APPLICATION NUMBER: US/09/712,495
; CURRENT FILING DATE: 2000-11-14
; PRIOR APPLICATION NUMBER: 09/062,440
; PRIOR FILING DATE: 1998-04-17
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 574
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-712-495-4

Query Match 97.7%; Score 505; DB 4; Length 574;
Best Local Similarity 94.9%; Pred. No. 1.7e-53;
Matches 93; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
Qy 1 WTCPCDKKAPYSLIIDGLFMEILXSCDCDEIQFMEDGSLWPKPKKEASEVCPPPGY 60
Db 310 WTCPCDKKAPYSLIIDGLFMEILXSCDCDEIQFMEDGSLWPKPKKEASEVCPPPGY 369
Qy 61 GLDGLQSPVQGGPSENKKKVEIDLTISSDEEDL 98
Db 370 GLDGLQSPVQGGPSENKKKVEIDLTISSDEEDL 407

RESULT 6
US-09-286-132-2
; Sequence 2, Application US/09286132
; Patent No. 6242185
; GENERAL INFORMATION:
; APPLICANT: Kaser, Matthew, R.
; APPLICANT: Baughn, Mariah, R.
; TITLE OF INVENTION: TRANSCRIPTION FACTOR REGULATORY PROTEIN
; FILE REFERENCE: PC-0001 US
; CURRENT APPLICATION NUMBER: US/09/286,132
; CURRENT FILING DATE: 1999-04-01
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PERL Program
; SEQ ID NO 2
; LENGTH: 628
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE: -
; OTHER INFORMATION: 2667068
US-09-286-132-2

Query Match 97.7%; Score 505; DB 3; Length 628;
Best Local Similarity 94.9%; Pred. No. 1.9e-53;
Matches 93; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
Qy 1 WTCPCDKKAPYSLIIDGLFMEILXSCDCDEIQFMEDGSLWPKPKKEASEVCPPPGY 60
Db 364 WTCPCDKKAPYSLIIDGLFMEILXSCDCDEIQFMEDGSLWPKPKKEASEVCPPPGY 423
Qy 61 GLDGLQSPVQGGPSENKKKVEIDLTISSDEEDL 98
Db 424 GLDGLQSPVQGGPSENKKKVEIDLTISSDEEDL 461

RESULT 7
US-09-836-941-2
; Sequence 2, Application US/09836941
; Patent No. 6465200
; GENERAL INFORMATION:
; APPLICANT: Kaser, Matthew, R.
; APPLICANT: Baughn, Mariah, R.
; TITLE OF INVENTION: TRANSCRIPTION FACTOR REGULATORY PROTEIN
; FILE REFERENCE: PC-0001 US
; CURRENT APPLICATION NUMBER: US/09/836,941
; CURRENT FILING DATE: 2001-04-17
; PRIOR APPLICATION NUMBER: 09/286,132
; PRIOR FILING DATE: 1999-04-01
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PERL Program
; SEQ ID NO 2
; LENGTH: 628
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE: -
; OTHER INFORMATION: 2667068
US-09-836-941-2

Query Match 97.7%; Score 505; DB 4; Length 628;
Best Local Similarity 94.9%; Pred. No. 1.9e-53;
Matches 93; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
Qy 1 WTCPCDKKAPYSLIIDGLFMEILXSCDCDEIQFMEDGSLWPKPKKEASEVCPPPGY 60
Db 364 WTCPCDKKAPYSLIIDGLFMEILXSCDCDEIQFMEDGSLWPKPKKEASEVCPPPGY 423
Qy 61 GLDGLQSPVQGGPSENKKKVEIDLTISSDEEDL 98
Db 424 GLDGLQSPVQGGPSENKKKVEIDLTISSDEEDL 461

RESULT 8
US-09-062-440-10
; Sequence 10, Application US/09062440
; Patent No. 6207422
; GENERAL INFORMATION:
; APPLICANT: Brown, Arthur M.
; APPLICANT: Yang, Qing
; APPLICANT: Wible, Barbara A.
; TITLE OF INVENTION: A Protein that Enhances Expression of Potassium Channels on Cell Surfaces
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Calfee, Halter & Griswold LLP
; STREET: 1400 McDonald Investment Center, 800 Superior
; CITY: Cleveland
; STATE: Ohio
; COUNTRY: US
; ZIP: 44114
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/09/062,440
; APPLICATION NUMBER: US/09/062,440
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Docherty, Pamela A.
; REGISTRATION NUMBER: 40591
; REFERENCE/DOCKET NUMBER: 22884/04004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 2162228200
; TELEFAX: 2162410816
; INFORMATION FOR SEQ ID NO: 10:

```

; SEQUENCE CHARACTERISTICS:
; LENGTH: 98 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 25..26
; OTHER INFORMATION: /note= "serine or asparagine"
;
; NAME/KEY: Peptide
; LOCATION: 61..62
; OTHER INFORMATION: /note= "glycine or glutamic acid"
;
; NAME/KEY: Peptide
; LOCATION: 63..64
; OTHER INFORMATION: /note= "aspartic acid or asparagine"
;
; NAME/KEY: Peptide
; LOCATION: 64..65
; OTHER INFORMATION: /note= "proline or glutamine"
;
; NAME/KEY: Peptide
; LOCATION: 70..71
; OTHER INFORMATION: /note= "lysine or arginine"
;
; US-09-062-440-10
;
; Query Match 97.5%; Score 504; DB 3; Length 98;
; Best Local Similarity 99.0%; Pred. No. 2.3e-54;
; Matches 97; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
;
; QY 1 WTCPCVCDKAPYESIIDGLFNEILXSCSDCEIQFMEDGSLWPKPKKEASEVCPFGY 60
; DB 1 WTCPCVCDKAPYESIIDGLFNEILXSCSDCEIQFMEDGSLWPKPKKEASEVCPFGY 60
;
; QY 61 GLDGLQYSPVQXGXPSENKXVEVIDLTIESSSDEEDL 98
; DB 61 GLDGLQYSPVQXGXPSENKXVEVIDLTIESSSDEEDL 98
;
; RESULT 9
; US-09-062-440-6
; Sequence 6, Application US/09062440
; Patent No. 6207422
; GENERAL INFORMATION:
; APPLICANT: Brown, Arthur M.
; APPLICANT: Yang, Qing
; APPLICANT: Wible, Barbara A.
; TITLE OF INVENTION: A protein that Enhances Expression of
; TITLE OF INVENTION: Potassium Channels on Cell Surfaces
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Calfee, Halter & Griswold LLP
; STREET: 1400 McDonald Investment Center, 800 Superior
; CITY: Cleveland
; STATE: Ohio
; COUNTRY: US
; ZIP: 44114
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/062,440
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Docherty, Pamela A.
; REGISTRATION NUMBER: 40591
;
; REFERENCE/DOCKET NUMBER: 22884/04004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 2162282200
; TELEFAX: 2162410816
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 574 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 37..38
; OTHER INFORMATION: /note= "glycine or serine"
;
; NAME/KEY: Peptide
; LOCATION: 41..42
; OTHER INFORMATION: /note= "proline or serine"
;
; NAME/KEY: Peptide
; LOCATION: 48..49
; OTHER INFORMATION: /note= "alanine or threonine"
;
; NAME/KEY: Peptide
; LOCATION: 115..116
; OTHER INFORMATION: /note= "valine or leucine"
;
; NAME/KEY: Peptide
; LOCATION: 335..336
; OTHER INFORMATION: /note= "serine or asparagine"
;
; NAME/KEY: Peptide
; LOCATION: 381..382
; OTHER INFORMATION: /note= "glycine or glutamic acid"
;
; NAME/KEY: Peptide
; LOCATION: 383..384
; OTHER INFORMATION: /note= "aspartic acid or asparagine"
;
; NAME/KEY: Peptide
; LOCATION: 384..385
; OTHER INFORMATION: /note= "isoproline or glutamine"
;
; NAME/KEY: Peptide
; LOCATION: 390..391
; OTHER INFORMATION: /note= "lysine or arginine"
;
; NAME/KEY: Peptide
; LOCATION: 416..417
; OTHER INFORMATION: /note= "serine or proline"
;
; NAME/KEY: Peptide
; LOCATION: 431..432
; OTHER INFORMATION: /note= "valine or alanine"
;
; NAME/KEY: Peptide
; LOCATION: 451..452
; OTHER INFORMATION: /note= "glycine or serine"
;
; NAME/KEY: Peptide
; LOCATION: 489..490
; OTHER INFORMATION: /note= "glycine or serine"
;
; NAME/KEY: Peptide
; LOCATION: 501..502
; OTHER INFORMATION: /note= "alanine or threonine"
;
; NAME/KEY: Peptide
; LOCATION: 508..509
; OTHER INFORMATION: /note= "alanine or threonine"
;

```

GenCore version 5.1.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 25, 2004, 01:30:24 ; Search time 14.8056 Seconds
(without alignments)
2018.720 Million cell updates/sec

Title: US-10-075-074-2
Perfect score: 3044
Sequence: 1 MKIKELYRRFRKTLGPSD.....GFLPGSLTGCSDVISLD 574

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2944	96.7	619	PIA3_HUMAN	Q9Y6x2 homo sapien
2	2749.5	90.3	584	PIA3_MOUSE	O54714 mus musculus
3	1636.5	53.8	651	PIA1_MOUSE	O88907 mus musculus
4	1621.5	53.3	651	PIA1_HUMAN	O75925 homo sapien
5	987.5	32.4	510	PIA2_HUMAN	O8n2w9 homo sapien
6	975	32.0	507	PIA2_MOUSE	Q9Ym05 mus musculus
7	263	8.6	726	NFIL1_YEAST	Q12216 saccharomyc
8	145.5	4.8	5262	MLL2_HUMAN	O14686 homo sapien
9	142	4.7	1509	GSRI_HUMAN	Q9nzm4 homo sapien
10	133.5	4.4	1329	KF10_HUMAN	Q9p218 homo sapien
11	129.5	4.3	1822	ZAP3_HUMAN	P49750 homo sapien
12	128.5	4.2	5147	PCLO_HUMAN	Q9Y6v0 homo sapien
13	127	4.2	5038	PCLO_MOUSE	Q9gyx7 mus musculus
14	126	4.1	1152	MAP4_HUMAN	P27816 homo sapien
15	125.5	4.1	3866	HRX_MOUSE	P52000 mus musculus
16	125	4.1	893	DAG1_MOUSE	Q62165 mus musculus
17	123.5	4.1	1257	PCGN_RAT	P55067 rattus norv
18	122	4.0	895	DAG1_BOVIN	O18738 bos taurus
19	121.5	4.0	931	MRTA_HUMAN	Q969v6 homo sapien
20	121	4.0	1324	IRS2_HUMAN	Q9Y4h2 homo sapien
21	120.5	4.0	1072	MAP4_BOVIN	P36225 bos taurus
22	120	3.9	789	ATX1_RAT	Q63540 rattus norv
23	119.5	3.9	964	MRTA_MOUSE	O8K4j6 mus musculus
24	119	3.9	487	EBN2_EBV	P12978 Epstein-bar
25	119	3.9	1048	Z217_HUMAN	O75362 homo sapien
26	118.5	3.9	1003	MEB6_HUMAN	Q96dnc homo sapien
27	118.5	3.9	1199	P121_RAT	P52591 rattus norv
28	118	3.9	1088	MRTB_HUMAN	Q9ulh7 homo sapien
29	118	3.9	1386	ZAP3_MOUSE	Q9r0i7 mus musculus
30	118	3.9	1567	FMN2_MOUSE	Q9Jl04 mus musculus
31	118	3.9	4911	MLL3_HUMAN	Q8ne4a homo sapien
32	117	3.8	1300	SAL3_HUMAN	Q9bxa9 homo sapien
33	116.5	3.8	1077	C3G_HUMAN	Q13905 homo sapien

34	116.5	3.8	1142	1	KPC1_NEUCR	P87253 neurospora
35	116.5	3.8	2688	1	ZEB1_MOUSE	Q03172 mus musculus
36	116.5	3.8	5179	1	MUC2_HUMAN	Q02817 homo sapien
37	116	3.8	895	1	GNDS_RAT	Q03386 rattus norv
38	115.5	3.8	484	1	IRX5_MOUSE	Q91kq4 mus musculus
39	115	3.8	1268	1	PGCN_MOUSE	P55066 mus musculus
40	113.5	3.7	649	1	V70K_EPMV	P20129 egplant mo
41	113.5	3.7	1323	1	SAL3_MOUSE	Q62255 mus musculus
42	113.5	3.7	1484	1	CES2_HUMAN	Q9bxf3 homo sapien
43	113.5	3.7	1744	1	TENS_CHICK	Q04205 gallus gall
44	113.5	3.7	2364	1	PGCA_BOVIN	P13608 bos taurus
45	113	3.7	1050	1	ULK1_HUMAN	O75385 homo sapien

ALIGNMENTS

RESULT 1
PIA3_HUMAN
ID PIA3_HUMAN STANDARD; PRT; 619 AA.
AC Q9Y6x2; Q9UFI3;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Protein inhibitor of activated STAT protein 3.
GN PIA33.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=9253144; PubMed=10319586;
RA Naka N, Seki N, Yano K, Saito T, Masuho Y, Muramatsu M;
RT "Isolation and chromosomal assignment of a human gene encoding protein
inhibitor of activated STAT3 (PIA33).";
RL J. Hum. Genet. 44:193-196(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood, and Muscle;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bonifard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Butterfield J.S.N., Krzywinski M.I., Skalska U., Smalls D.E.,
Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [3]
RP SEQUENCE OF 301-619 FROM N.A.
RC TISSUE=Breast cancer;
RA Poustka A., Klein M., Mewes H.-W., Gassenhuber J., Wiemann S.;
Submitted (Oct-1999) to the EMBL/GenBank/DBJ databases.
CC -I- FUNCTION: Specifically inhibits activated STAT3 signaling by
blocking its DNA-binding activity.
CC -I- SUBCELLULAR LOCATION: Nuclear (By similarity).
CC -I- TISSUE SPECIFICITY: Widely expressed.
CC -I- SIMILARITY: Contains 1 SAP domain.
CC -I- SIMILARITY: Contains 1 MIZ-type zinc finger.

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CC		-----	
DR	EMBL; AB021868;	BAA78533.1; -	
DR	EMBL; BC001154;	AAR01154.1; -	
DR	EMBL; BC030556;	AAH30556.1; -	
DR	EMBL; AL122061;	CAB59241.1; -	
DR	PIR; T34525;	T34525.	
DR	MIM; 605987;	-	
DR	InterPro; IPR003034;	SAP.	
DR	InterPro; IPR004181;	Znf_MIZ.	
DR	Pfam; PF02037;	SAP; 1.	
DR	Pfam; PF02891;	zf-MIZ; 1.	
DR	SMART; SM00513;	SAP; 1.	
DR	PROSITE; PS50800;	SAP; 1.	
KW	Zinc-finger; Nuclear protein.	SAP.	
FT	DOMAIN	2	36
FT	ZN FING	314	366
SO	SEQUENCE	619 AA; 67008 MW;	A749A877D8925AC7 CRC64; MIZ-TYPE.

Query Match	96.7%	Score 2944;	DB 1;	Length 619;
Best Local Similarity	96.3%	Pred. No. 1.7e-184;		
Matches 553;	Conservative	7;	Mismatches 14;	Indels 0;
Gaps 0;				

Qy	1	KKIKELVRRRPRKTLGSPDSL	SLSLSPGTSVPGSPGLASIPPTLT	TPGTLLPGKREVD	60
Db	46	MKIKELVRRRPRKTLGSPDSL	SLSLSPGTSVPGSPGLAPIPPTLL	APGTLPGKREVD	105
Qy	61	MHPPLPQVHPDVTWKPLPF	VEYVGELIRPTTLASTSORFEEAHF	FALTPQOLQOILT	120
Db	106	MHPPLPQVHPDVTWKPLPF	VEYVGELIRPTTLASTSORFEEAHF	FALTPQOVQOILT	165
Qy	121	SREVLPGAKCDYTIQVLR	FCFLCETSCPOEDYFPNLFVKVNGKLC	PLPGYLPPTKNGAE	180
Db	166	SREVLPGAKCDYTIQVLR	FCFLCETSCPOEDYFPNLFVKVNGKLC	PLPGYLPPTKNGAE	225
Qy	181	PKRPSRPINITPLARLSAT	VPNTIVVMSSBFGNYSLSVYLVRQL	TAGTTLQKLRAKGI	240
Db	226	PKRPSRPINITPLARLSAT	VPNTIVVMSSBFGNYSLSVYLVRQL	TAGTTLQKLRAKGI	285
Qy	241	RNPDSRALIKEKLTADPDS	EVATTSLRVSIMCPLGKMRLTVPCAL	TCAHLQSFDAALY	300
Db	286	RNPDSRALIKEKLTADPDS	EVATTSLRVSIMCPLGKMRLTVPCAL	TCAHLQSFDAALY	345
Qy	301	LQMEKKPTWTCPVCDK	KAPYESLIIDGLFMEILN	SCSDCDEIQMEDGSCWPKPKKEA	360
Db	346	LQMEKKPTWTCPVCDK	KAPYESLIIDGLFMEILN	SCSDCDEIQMEDGSCWPKPKKEA	405
Qy	361	SEVCPPPGYGLDGLQY	SPVQEGNQSENKKRVEVIDLT	TISSSDEBDLPTTKHCPVTGAA	420
Db	406	SEVCPPPGYGLDGLQY	SPVQEGDPSENKKVEVIDLT	TISSSDEBDLPTTKHCSVTGAA	465
Qy	421	IPALPGSKALTSCHQPS	SVLRSAMWGTGSDFLSSLP	LHYEPPAFPLGADIQGLDLSF	480
Db	466	IPALPGSKGLVTSCHQ	PSVLSAMWGTGGDFLSSLP	LHYEPPAFPLGADIQGLDLSF	525
Qy	481	LOTESQHSYSPVITSL	DEODTLGHFPQFRGTPPHFLG	PLAPTLGSSSHRSATPAPAGRVS	540
Db	526	LOTESQHGYPVITSL	DEODALGHFQYRGTPSHEL	GPLAPTLGSSSHCSATPAPPPGRVS	585
Qy	541	STVAPGSSLREHG	GGPLPGSPSLTGCRSDV	ISLD	574
Db	586	STVAPGALREHG	GGPLPGSPSLTGCRSDI	ISLD	619

RESULT 2	
PIA3_MOUSE	
ID_PIA3_MOUSE	STANDARD;
	PRT; 584 AA.

PRT; 584 AA.

PIA3_MOUSE
ID_PIA3_MOUSE

```

AC OS44714;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Protein inhibitor of activated STAT protein 3.
DE PIAS3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutharia; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RN SEQUENCE FROM N.A.
RM MEDLINE=98049615; PubMed=9388184;
RA Chung C.D., Liao J., Liu B., Rao X., Jay P., Berta P., Shuai K.;
RT Specific inhibition of Stat3 signal transduction by PIAS3."
RL Science 278.1803-1805(1997)
CC -1- FUNCTION: Specifically inhibits activated STAT3 signaling by
CC blocking its DNA-binding activity.
CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).
CC -1- SIMILARITY: Contains 1 SAP domain.
CC -1- SIMILARITY: Contains 1 MIZ-type zinc finger.
CC
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CC -----
DR EMBL; AF034080; AAB88902.2; -.
DR MGD; MGI:1913126; Pias3.
DR InterPro; IPR003034; SAP.
DR InterPro; IPR004181; Znf_MIZ.
DR Pfam; PF02037; SAP; 1.
DR Pfam; PF02891; zf-MIZ; 1.
DR SMART; SMC0513; SAP; 1.
DR PROSITE; PS50800; SAP; 1.
DR Zinc-finger; Nuclear protein.
DR DOMAIN 2 36 SAP.
FT FT 279 331
FT ZN FING 279 331 MIZ-TYPE.
SO SEQUENCE 584 AA; 636552 MW; 8567831ACAD0D098 CRC64;

```

Query Match	90.3%	Score 2749.5	DB 1	Length 584
Best Local Similarity	91.3%	Pred. No. 7.5e-172		
Matches 524	Conservative	5	Mismatches 10	Indels 35
Matches 524	Conservative	5	Mismatches 10	Indels 35

QY		1	MKIKELYRRRFPKRKTIGPSDLSSLSLPPGTSIPVSGSPSLASIPPTLLTPGTLLPGPKREVD	60
Dd		46	MKIKELYRRRFPKRKTIGPSDLSSLSLPPGTSIP	77
QY		61	MHPPLPOVPHDVTMKPLPFYEVVGELIRPTTLLASTSSORFEEAHFTFALTPOOLQILIT	120
Dd		78	-----PVHPPDVMTKPLPFYEVVGELIRPTTLLASTSSORFEEAHFTFALTPOOLQILIT	133
QY		121	SREVLPGAACDYTTIQVOLRCLCETSCPBEDYFPNLFVKVNGKLCPLPGVLPPTKGAE	180
Dd		131	SREVLPGAACDYTTIQVOLRCLCETSCPBEDYFPNLFVKVNGKLCPLPGVLPPTKGAE	190
QY		181	PKRSRPINITPLARLSATVNTIIVNWSSEFGFNYSLSVYLVRQLTAGTLLOKLRAKI	240
Dd		191	PKRSRPINITPLARLSATVNTIIVNWSSEFGFNYSLSVYLVRQLTAGTLLOKLRAKI	250
QY		241	RNPDSRALIKEKITADPDSVAATTSLRVSLMCPLGKMRLTVPCRALTC AHLQSFDAALY	300
Dd		251	RNPDSRALIKEKITADPDSVAATTSLRVSLMCPLGKMRLTVPCRALTC AHLQSFDAALY	310
QY		301	LQMNKKPTWTCPCVCDKAPYESLIIDGLFMFIINLNSCDDCEIOFMEDGSCMPKPKEA	360
Dd		311	LQMNKKPTWTCPCVCDKAPYESLIIDGLFMFIINLNSCDDCEIOFMEDGSCMPKPKEA	370
QY		361	SEVCPPPGLDGLQYSPVOGNQSENKKRVEVTDLTIESSDDEEDLPPTKKHCPCVTSAA	420

```

RESULT 3.
P1AL MOUSE STANDARD; PRT; 651 AA.
O88907;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
DE Protein inhibitor of activated STAT protein 1 (DEAD/H box binding
protein 1).
DE P1AS1 OR DDXBP1.
GN Mus musculus (Mouse).
OS Eukaryota; Metazoa; Chordata; Vertebrata; Eutelestomii;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
[1]
SEQUENCE FROM N.A.
TISSUE=B-cell;
MEDLINE=98393695; PubMed=9724754;
Liu B., Liao J., Rao X., Kushner, S.A., Chung C.D., Chang D.D.,
Shuai K.;
" Inhibition of Stat1-mediated gene activation by PIAS1. ";
Proc. Natl. Acad. Sci. U.S.A. 95:10626-10631(1998).
- !- FUNCTION: Specifically inhibits activated STAT1 signaling by
blocking its DNA-binding activity.
- !- SUBCELLULAR LOCATION: Nuclear (By similarity).
- !- SIMILARITY: Contains 1 SAP domain.
- !- SIMILARITY: Contains 1 Miz-type zinc finger.
-----
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-----
EMBL; AF077950; AAC36701.1; -
MGD; MGI:1913125; Pias1.
InterPro; IPR003034; SAP.
InterPro; IPR004181; Znf_MIZ.
Pfam; PF02037; SAP; 1.
Pfam; PF02891; zf-MIZ; 1.
SMART; SM00513; SAP; 1.
PROSITE; PS50800; SAP; 1.
Repeat; Zinc-finger; Nuclear protein.
DOMAIN 11 45
FT ZN FING 331 383 MIZ-TYPE.
FT DOMAIN 56 64 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
FT DOMAIN 368 380 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
FT DOMAIN 577 634 SER-RICH.
FT DOMAIN 520 615 4 X 4 AA REPEATS OF N-T-S-L.
FT REPEAT 520 523 1.
FT REPEAT 557 560 2.
FT REPEAT 598 601 3 (APPROXIMATE).
FT REPEAT 612 615 4 (APPROXIMATE).
SEQUENCE 651 AA; 71607 MW; DBD544128E817C81 CRC64;
53.8%; Score 1636.5; DB 1; Length 651;
Query Match

```

Best Local Similarity 57.3%; Pred. No. 2.6e-39;
Matches 349; Conservative 79; Mismatches 134; Indels 47; Gaps 19;

QY	1	MKIKELRRRFRKTLGSDLSLTS-----LPPTSPVSGPSPL-----ASIPPTLLTPG	50
Db	55	MKIKELRRRFPQKINTPADLSIPNVHSSPMTLSPSTIQUTDGHPPASSP---LLPV	111
QY	51	TALGPKREVDMHPPLP--QPVRPDVTMKPLPEYEVYGELIRPTTILASTSORFEEAHFT	107
Db	112	SLLGPKHELEL-PHLTSALHPVHPDIKLQKLPYDLLDELIKETSLASDNSQRFTCF	170
QY	108	FALTFOOLOOIIITSREVLFGAKDYTIQVLRCLCETSCPOBDYPDPNLFVKVNGKLCP	167
Db	171	FALTFOOVQOIISSMMDI-SGTCKDFTVQVQLRFCLSETSCPQSDHFPPNLGVNTKPCS	229
QY	168	LPGYLPTTKNGAEKPSPINITPLARLSATVPNTIVVNSSEFGRNYSLSVLYAVRLT	227
Db	230	LPGYLPTTKNGVEPKKSPINITSVLRLSTVNTIVVSWTAIEIGRTYSMAVILVKQLS	289
QY	228	AGTLQKLEAKGRINPDHSRALIKEKITADPDSEVATTSLRVSLMCPGLGMRLTVP	287
Db	290	STVLLQRLFAKGRINPDHSRALIKEKITADSDSEIATTSLRVSLLCPLGKMRLTIPC	349
QY	288	TCAILQSPDAALYLQNEKKPTWPCVDKKAPYESLIIDGLFMETILNCSDCDEIQFME	347
Db	350	TCSHLQCDFATYIOWNEKKPTWPCVDKKAPYEHLIIDGLFMETILKYCTDCDEIQFXE	409
QY	348	DGSWCMPKFKKEASEVCPPGY-GLDGLQYS----PVQSGNQSENK-KRVEVIDLTIES	401
Db	410	DGSWAPMRSKSRQVEV--TASVNGVDGCLSTLEHQVAHNSNNKKVVEIDLTDISS	467
QY	402	SD-EEDLPPTKKHCPTSAAIPALPGSKGALTSGHOPSVLVRSPPAMGTILGSDFLSLPLH	450
Db	468	SDEEEEPKACTCSLSSTSPL--SNKGILSLPHQASPVRTPSIPAVDTSVINTSLIQ	525
QY	461	EYPPAF----PLGADIQGLDLFSFLQTESQHYSPTSITSL-----DEQDTL--GHFFQFRG	510
Db	526	DYRHHPHTMPFYDLQGLDFPFPLSGDNQHYNTSLIAAAAAAASDDQDLLHSSRFFPYTS	585
QY	511	TPPHLGPLAPTLLGSHRSATAPAPGRVSSIVAPCGSSLREGHGGLPS-----GPSLTG	565
Db	586	S-QMFDLQLDSAG-GSTSLPATNGSSSGNSSILVS--SNSLRSHGHGVASRSSADTASIFG	642
QY	566	CRSDVISILD 574	
Db	643	IIPDIISLD 651	

RESULT 4
PIAL HUMAN STANDARD; PRT; 651 AA.

AC	O75925; Q99751; Q9UN02;	
DT	28-FEB-2003 (Rel. 41, Created)	
DT	28-FEB-2003 (Rel. 41, Last sequence update)	
DE	28-FEB-2003 (Rel. 41, Last annotation update)	
DE	Protein inhibitor of activated STAT protein 1 (Gu binding protein) (GBP) (RNA helicase II binding protein) (DEAD/H box-binding protein PIAS1 OR DDXBP1.	
GN	PIAS1 OR DDXBP1.	
OS	Homo sapiens (Human).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
NCBI_TaxId=9606;		
[1]		
RN	SEQUENCE FROM N.A., AND FUNCTION.	
RP	TISSUE=B-cell;	
RC	MEDLINE=98393695; PubMed=9724754;	
RR	Liu B., Liao J., Rao X., Kushner S.A., Chung C.D., Chang D.D.,	
RA	Shuai K.;	
RA	"Inhibition of Stat1-mediated gene activation by PIAS1."	
RT	Proc. Natl. Acad. Sci. U.S.A. 95:10626-10631(1998).	
RL	[2]	
RN	SEQUENCE FROM N.A.	
RP		

RX MEDLINE=2009325; PubMed=10628744;
 RA Tan J., Hall S.H., Hamil K.G., Grossman G., Petrusz P., Liao J.,
 RA Shuai K., French F.S.;
 RT "Protein inhibitor of activated STAT-1 (signal transducer and
 RT activator of transcription-1) is a nuclear receptor coregulator
 RT expressed in human testis";
 RL Mol. Endocrinol. 14:14-26(2000).
 RN [3].
 RP SEQUENCE OF 7-650 FROM N.A., SUBCELLULAR LOCATION, AND TISSUE
 RP SPECIFICITY.
 RC TISSUE=B-cell;
 RX MEDLINE=97320420; PubMed=9177271;
 RA Valdez B.C., Henning D., Parlay L., Busch R.K., Busch H.;
 RT "Cloning and characterization of Gu/RH-II binding protein";
 RL Biochem. Biophys. Res. Commun. 234:335-340(1997).
 CC -!- FUNCTION: Specifically inhibits activated STAT1 signaling by
 CC blocking its DNA-binding activity.
 CC -!- SUBUNIT: Binds p53, RNA helicase II and androgen receptor.
 CC -!- SUBCELLULAR LOCATION: Nuclear.
 CC -!- TISSUE SPECIFICITY: Highly expressed in testis.
 CC -!- SIMILARITY: Contains 1 SAP domain.
 CC -!- SIMILARITY: Contains 1 MIZ-type zinc finger.
 CC
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 CC
 DR EMBL; AF077951; AAC36702.1; --
 DR EMBL; AF167160; AAD49722.1; --
 DR EMBL; U78524; AAB58488.1; --
 DR Genew; HGNC:2752; PIAS1.
 DR MIM; 603566; --
 DR GO; GO:0005634; C:nucleus; TAS.
 DR GO; GO:0003714; F:transcription co-repressor activity; TAS.
 DR GO; GO:0007255; P:JAK-STAT cascade; TAS.
 DR InterPro; IPR003034; SAP.
 DR InterPro; IPR004181; ZnF_MIZ.
 DR Pfam; PF02037; SAP; 1.
 DR Pfam; PF02891; zf-MIZ; 1.
 DR SMART; SM00513; SAP; 1.
 DR PROSITE; PS00800; SAP; 1.
 KW Repeat; Zinc-finger; Nuclear protein.
 FT DOMAIN 11 45
 FT ZN_FING 331 383
 FT MIZ-TYPE.
 FT DOMAIN 56 64
 FT NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
 FT DOMAIN 368 380
 FT NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
 FT DOMAIN 577 634
 FT SER-RICH
 FT DOMAIN 520 615
 FT 4 X 4 AA REPEATS OF N-T-S-L.
 FT REPEAT 520 523
 FT 1.
 FT REPEAT 557 560
 FT 2.
 FT REPEAT 598 601
 FT 3 (APPROXIMATE).
 FT REPEAT 612 615
 FT 4 (APPROXIMATE).
 FT CONFLICT 119 119
 FT E K (IN REF. 1).
 FT CONFLICT 266 268
 FT YV -> T (IN REF. 1).
 FT CONFLICT 613 613
 FT S -> T (IN REF. 3).
 FT SEQUENCE 651 AA; 71835 MW; AA69338221124119 CRC64;

Query Match
 Best Local Similarity 53.3%; Score 1621.5; DB 1; Length 651;
 Matches 346; Conservative 82; Mismatches 131; Indels 53; Gaps 20;

Qy 1 MKIKELRRRFRKTLGSPDLN-----LSLPPGTSVP-----GSPSPASIPPTLL 47
 Db 55 MKIKELRRRFRKTLGSPDLN-----LSLPPGTSVP-----GSPSPASIPPTLL 108
 Qy 48 TPGTLLGPKREVDMEHPLP---QVHPDVTMKPLPEYVGVGLIRPTTLASTSSOREEA 104
 Db 109 LPVSLGPKHELEL-PHLTSLALHPVHPDIKQLKPLFPYDLLEIKPTSLASDNSQRFRT 167

Qy 105 HFTALTPQOQLTQREVLPKAGKDYTIQVQLRFLCICETSCQEDYFPFNLVFKVNGK 164
 Db 168 CFALPTPQQVQQLSSMDI-SGTKCDFTVQVQLRFLCICETSCQEDHFPENLCKVNTK 226
 Qy 165 LCPLPGYLPPTKGAEPKRPSPINITPLARLSATVNTIVNWSSEFGNYSLSVLVR 224
 Db 227 PCSLPGYLPPTKNGVEPKRPSPINITSVRLSTTVPNTIVSWTAIGRNYMAVLVK 286
 Qy 225 QLTAGTLLQKLRAGIRNPDHRSRALIKEKLTADPDSEVATSLRVSMLCPGKRLTTPC 284
 Db 287 QLSSTVILLQRLRAKIRNPDHRSRALIKEKLTADPDSEIATSLRVSLLCPGKRLTTPC 346
 Qy 285 RALTCAHLQSFDAALYLQMEKKPTWTCPVCKKAPYESLIIDGLFMEILNSCSDCDRIQ 344
 Db 347 RALTCSHLQCFDAILYQMEKKPTWTCPVCKKAPYEHLLIIDGLFMEILAYCTDCDRIQ 406
 Qy 345 FMEDGSCWCPMKPKKAESEVCPPOY-GLDGLQYS-----PVQGNQSENK-KRVEIDITLI 398
 Db 407 FKEDGTWAPMRKKEVOEV--SASVNGVDGCLSTLEHQAASHHQSNNKKNKVEIDITLI 464
 Qy 399 BSSSDEEDLPPT-KKHCPTVSAATPALPGSKGALTSGHOPSSVLRSPAMGTLSGLSSSL 457
 Db 465 DSSSDEEEPSAKRTCPSLSTPL--NNAGILSLPHQAQSPVSRIPSLPAVDTSYINTS 522
 Qy 458 PLHEYPPAF---PLGADIQGLDLFSFLQTESQHYSPSVITSL-----DEODTL--GHFPQ 507
 Db 523 LIQYRHPFMTWPDYDGLDFPFLSGDNQHYNTSLAAAAAASVDDQLHSSRFFP 582
 Qy 508 FRGTPPHPLGLPLATLSSSHRSATPAPAGRVSSIVAPGSLRGHGGPLFS-----GPS 562
 Db 583 YTSS-QMFLDQLSAG-GSTSLFTTNGSSGSSNLSVS-SNSLRSHSHSTVTRNSSTDAS 639
 Qy 563 LTGCRSDVISLD 574
 Db 640 IFGIIPDIISLD 651
 RESULT 5
 ID PIAG_HUMAN STANDARD; PRT; 510 AA.
 AC Q8N2W9; O75926; Q96G19; Q9UNI6;
 DT 10-OCT-2003 (Rel. 42, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Protein inhibitor of activated STAT protein gamma (PIAS-gamma)
 DE (PIASy).
 GN PIASG.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=B-cell;
 RX MEDLINE=98393695; PubMed=9724754;
 RA Liu B., Liao J., Rao X., Kushner S.A., Chung C.D., Chang D.D.,
 RA Shuai K.;
 RT "Inhibition of Stat1-mediated gene activation by PIAS1";
 RL Proc. Natl. Acad. Sci. U.S.A. 95:10626-10631(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain, Lung, and Skin;
 RX MEDLINE=23384925; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Prange C.,
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Schaefer T.E.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

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OM protein - protein search, using sw model

Run on: August 25, 2004, 01:30:24 ; Search time 14.8056 seconds
(without alignments)
2018.720 Million cell updates/sec

Title: US-10-075-074-4
Perfect score: 3056
Sequence: 1 MKIKLYRRFRPKTLGPSD.....GFLPSPSLTGCRSDIISLD 574

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3056	100.0	619	PIA3 HUMAN	Q9Y6X2 homo sapien
2	2718.5	89.0	584	PIA3 MOUSE	O54714 mus musculus
3	1637.5	53.3	651	PIA1 MOUSE	O88907 mus musculus
4	1613.5	52.8	651	PIA1 HUMAN	O75925 homo sapien
5	994.5	32.5	510	PIA3 HUMAN	Q8N2W3 homo sapien
6	976	31.9	507	PIA3 MOUSE	Q9Jm05 mus musculus
7	268.5	8.8	726	NEF1 YEAST	Q12216 saccharomyc
8	152.5	5.0	1509	GSR1 HUMAN	Q9Nzm4 homo sapien
9	138.5	4.5	5262	MLL2 HUMAN	O14686 homo sapien
10	134.5	4.4	1003	MBD6 HUMAN	Q36dn6 homo sapien
11	130	4.3	638	2297 MOUSE	Q320G7 mus musculus
12	130	4.3	1152	NAP4 HUMAN	P27816 homo sapien
13	129	4.2	1300	SAL3 HUMAN	Q9bxa9 homo sapien
14	128.5	4.2	1072	NAP4 BOVIN	P36225 bos taurus
15	128.5	4.2	1134	SRE1 MOUSE	Q9Wtn3 mus musculus
16	125	4.1	487	EBN2 EBV	P12978 Epstein-bar
17	125	4.1	1484	CEB2 HUMAN	Q9bxf3 homo sapien
18	124.5	4.1	1329	KEF10 HUMAN	Q9P218 homo sapien
19	124	4.1	579	RELB HUMAN	Q01201 homo sapien
20	124	4.1	1844	POLR TYMV	P20128 turnip yell
21	124	4.1	5703	MU5B HUMAN	Q9hcd4 homo sapien
22	122	4.0	1516	CA1H HUMAN	P39060 homo sapien
23	122	4.0	5147	PCLO HUMAN	Q9Y6V0 homo sapien
24	121.5	4.0	2364	PCSA BOVIN	P33608 bos taurus
25	121	4.0	1567	FNW2 MOUSE	Q9J104 mus musculus
26	120	3.9	542	ZYX CHICK	Q04584 gallus gall
27	120	3.9	1077	C3G HUMAN	Q13905 homo sapien
28	119	3.9	634	2297 HUMAN	O15209 homo sapien
29	119	3.9	1257	PCGN RAT	P35067 rattus norv
30	119	3.9	1464	CA13 MOUSE	P08121 mus musculus
31	118	3.9	789	ATX1 RAT	Q63540 rattus norv
32	118	3.9	1574	SYJ1 RAT	Q62910 rattus norv
33	117.5	3.8	649	V70K EPMV	P20129 eggplant mo

34	117.5	3.8	2688	1	ZEPL MOUSE	Q03172 mus musculus
35	117	3.8	5038	1	PCLO MOUSE	Q9QYX7 mus musculus
36	116.5	3.8	1323	1	SAL3 MOUSE	Q82255 mus musculus
37	116.5	3.8	1822	1	ZAP3 HUMAN	P49750 homo sapien
38	116.5	3.8	1844	1	POLR TYMV	P10358 turnip yell
39	116	3.8	817	1	VRP1 YEAST	P37370 saccharomyc
40	116	3.8	895	1	GNDS RAT	Q03386 rattus norv
41	115.5	3.8	789	1	PRD1 HUMAN	O75626 homo sapien
42	115.5	3.8	3164	1	TEGU_HSV1	P10220 herpes simp
43	115	3.8	893	1	DAG1 MOUSE	Q62165 mus musculus
44	115	3.8	1132	1	BAT3 HUMAN	P46379 homo sapien
45	114.5	3.7	1844	1	POLR TYMVC	P28477 turnip yell

ALIGNMENTS

RESULT 1
PIA3 HUMAN
ID PIA3 HUMAN STANDARD; PRT; 619 AA.
AC Q9Y6X2; Q9UFI3;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Protein inhibitor of activated STAT protein 3.
GN PIA3
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]
RP SEQUENCE FROM N.A.
RX MEDLINE=9253144; PubMed=10319586;
RA Ueki N., Seki N., Yano K., Saito T., Masuho Y., Muramatsu M.;
RT "Isolation and chromosomal assignment of a human gene encoding protein
RT inhibitor of activated STAT3 (PIAS3).";
RL J. Hum. Genet. 44:193-196(1999).
[2]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood, and Muscle;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Colling F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A.C., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[3]
RP SEQUENCE OF 301-619 FROM N.A.
RC TISSUE=Breast cancer;
RA Poustka A., Klein M., Mewes H.-W., Gassenhuber J., Wiemann S.;
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Specifically inhibits activated STAT3 signaling by
CC blocking its DNA-binding activity.
CC -!- SUBCELLULAR LOCATION: Nuclear (By similarity).
CC -!- TISSUE SPECIFICITY: Widely expressed.
CC -!- SIMILARITY: Contains 1 SAP domain.
CC -!- SIMILARITY: Contains 1 MIZ-type zinc finger.

QY 361 SEVCPPGYGLDGLQYSPVQGGDPSRNNKKEVIDTIESDDEEDLPPTKKHCSTSA 420
: : : : :
311 LGNKKRFFWLCFVCUNAFIESLIIDGLDFRMLNSCSDCDEIYQFMEDGSGNCFKAKRNER 370
DU

RESULT 2	
PIA3 MOUSE	
ID PIA3 MOUSE	
STANDARD;	PRT; 584 AA.

Db 371 SEVCPPEGYGLDQYSAVQRIQPKKRVVEVIDLTIESSSDEEDLPPTKKHCPVTSAA 430
 Qy 421 IPALPGSKVLTSGHSPSSVLRSPAMGTGLGDFLSSPLPHYPPAPPLGADIQGLDLFSF 480
 Db 431 IPALPGSKGALTSGHSPSSVLRSPAMGTGLGDFLSSPLPHYPPAPPLGADIQGLDLFSF 490
 Qy 481 LQTESQHYGVSITSLDEQDALGHFFQVRGTPSHFLGLPAPTLGSSHCSTAPPPGGRVS 540
 Db 491 LQTESQHYGVSITSLDEQDALGHFFQVRGTPSHFLGLPAPTLGSSHCSTAPPPGGRVS 550
 Qy 541 SIVAPGALREGHGGLPSPGSLTGCSDIISLD 574
 Db 551 SIVAPGSLREGHGGLPSPGSLTGCSDIISLD 584

RESULT 3

PIAL_MOUSE STANDARD; PRT; 651 AA.
 ID PIAL_MOUSE
 AC 088907
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Protein inhibitor of activated STAT protein 1 (DEAD/H box binding protein 1).
 DE P1AS1 OR DDXBP1.
 GN Mus musculus (Mouse).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 RN [1]
 SEQUENCE FROM N.A.
 RP TISSUE=B-cell;
 RC MEDLINE=98393695; PubMed=9724754;
 RA Liu B., Liao J., Rao X., Kushner S.A., Chung C.D., Chang D.D., Shuai K.;
 RT "Inhibition of Stat1-mediated gene activation by P1AS1.";
 RL Proc. Natl. Acad. Sci. U.S.A. 95:10626-10631(1998).
 CC -!- FUNCTION: Specifically inhibits activated STAT1 signaling by blocking its DNA-binding activity.
 CC -!- SUBCELLULAR LOCATION: Nuclear (by similarity).
 CC -!- SIMILARITY: Contains 1 SAP domain.
 CC -!- SIMILARITY: Contains 1 Miz-type zinc finger.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.ebi.ac.uk/announcements> or send an email to license@sib-sib.ch).
 CC -----
 DR EMBL; AF077950; AAC36701.1; -.
 DR MGD; MGI:1913125; P1as1.
 DR InterPro; IPR003034; SAP.
 DR InterPro; IPR004181; Znf_MIZ.
 DR Pfam; PF02037; SAP; 1.
 DR Pfam; PF02891; zf-MIZ; 1.
 DR SMART; SM00513; SAP; 1.
 DR PROSITE; PS00800; SAP; 1.
 KW Repeat; Zinc-finger; Nuclear protein.
 FT DOMAIN 11 45
 FT ZN FING 331 383 MIZ-TYPE.
 FT DOMAIN 56 64 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
 FT DOMAIN 368 380 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
 FT DOMAIN 577 634 SER-RICH.
 FT DOMAIN 520 615 4 X 4 AA REPEATS OF N-T-S-L.
 FT REPEAT 520 523 1.
 FT REPEAT 527 560 2.
 FT REPEAT 557 560 1.
 FT REPEAT 598 601 3 (APPROXIMATE).
 FT REPEAT 612 615 4 (APPROXIMATE).
 FT REPEAT 651 AA; 71607 MW; DBD544128E817C81 CRC64;
 SQ SEQUENCE 53.3%; Score 1627.5; DB 1; Length 651;

Query Match

Best Local Similarity 56.8%; Pred. No. 2.8e-98;
 Matches 346; Conservative 75; Mismatches 141; Indels 47; Gaps 18;
 Qy 1 MKIKELVRRPRTKTPGSDLSLLS-----LPQTSVPVSGSP-----GFLAPIPPTLLAPG 50
 Db 55 MKIKELVRRPRTKTPGSDLSLLS-----LPQTSVPVSGSP-----GFLAPIPPTLLAPG 111
 Qy 51 TLGPKREVDHPLP---CPVHPDVTMKLPVVEYVGLIRPTTLASTSQREAEHFT 107
 Db 112 SLGPGHELEL-PHLTALPHVHPDIKLPFYDLDLDELKPTSLASDNSQRFETCF 170
 Qy 108 FALTPOQVOQLTSLREVLPGAKCDYTIQVQLFCLETSCPOEDYFPNLFVKVNGKLC 167
 Db 171 FALTPOQVOQLTSLREVLPGAKCDYTIQVQLFCLETSCPOEDYFPNLFVKVNGKLC 229
 Qy 168 LPGALETNGAEKPRSRPINITPLARLSATVENTIVANWSSSEFGNYSLSVYLRQLT 227
 Db 230 LPGALETNGAEKPRSRPINITPLARLSATVENTIVANWSSSEFGNYSLSVYLRQLT 289
 Qy 228 AGTLLQKLRAGIRNPDHSLALKEKLTADPDSEVATSLRVSLMCDLGMRLTVPCLAL 287
 Db 290 STVLLQKLRAGIRNPDHSLALKEKLTADPDSEVATSLRVSLMCDLGMRLTVPCLAL 349
 Qy 288 TCAHQSFDAALYLQNNKKPTWTCPCVCDKAPYESLIIDGLFWEILLSSGDCDEIOFME 347
 Db 350 TCSHLQCFDATALYQNNKKPTWTCPCVCDKAPYESLIIDGLFWEILLSSGDCDEIOFME 409
 Qy 348 DGSWCPMKPKKEASEVCPVPGY-GLDG-----LQYSPVQGGDPSENKKKVEVIDLTIES 401
 Db 410 DGSWCPMKPKKEASEVCPVPGY-GLDG-----LQYSPVQGGDPSENKKKVEVIDLTIES 467
 Qy 402 SD-EEDLPPTKKHCPVTSAAIPALPGSKVLTSGHSPSSVLRSPAMGTGLGDFLSSPLH 460
 Db 468 SDEEEEPKAKRTCPSLSPSPL--SNKGILSPHQASPVSRTPSLPAVDTSYINTSLIQ 525
 Qy 461 EYPPAF---PLGADIQGLDLFSFLQTSQHYGVSITSL-----DEQDAL--GHFFQVRG 510
 Db 526 DYRHPFHTMPYDYLQGLDFPFLSGDNQHYNTSLAAANVSDQDLHSSFFPYTS 585
 Qy 511 TPSHFLGLPAPTIGSSHCSTAPPPGGRVSIVAPGALREGHGGLPSP-----GPSLTG 565
 Db 586 S-QMFLDQLSAG-GSTSLPATNGSSGSSGSLNS-SNSRESHGSHGVASRSADTASIFG 642
 Qy 566 CRSDIISLD 574
 Db 643 IIPDIISLD 651
 RESULT 4
 PIAL_HUMAN STANDARD; PRT; 651 AA.
 ID PIAL_HUMAN
 AC 075925; Q99751; Q9UN02;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Protein inhibitor of activated STAT protein 1 (Gu binding protein) (GBP) (RNA helicase II binding protein) (DEAD/H box-binding protein 1).
 DE P1AS1 OR DDXBP1.
 GN Homo sapiens (Human).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 SEQUENCE FROM N.A., AND FUNCTION.
 RP TISSUE=B-cell;
 RC MEDLINE=98393695; PubMed=9724754;
 RX Liu B., Liao J., Rao X., Kushner S.A., Chung C.D., Chang D.D., Shuai K.;
 RA "Inhibition of Stat1-mediated gene activation by P1AS1.";
 RL Proc. Natl. Acad. Sci. U.S.A. 95:10626-10631(1998).
 RN [2]
 RP SEQUENCE FROM N.A.

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OM protein - protein search, using sw model

Run on: August 25, 2004, 01:30:24 ; Search time 2.55357 Seconds
(without alignments)
2018.720 Million cell updates/sec

Title: US-10-075-074-5

Perfect score: 544

Sequence: 1 TWTCPCVCKKAPVESLIIDG.....KKKVEVDLTIESSDDEDL 99

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	544	100.0	619	1	PIA3 HUMAN
2	495	91.0	584	1	Q9Y6X2 mouse
3	427	60.1	651	1	PIA3 MOUSE
4	322	59.2	651	1	PIA1 MOUSE
5	257.5	47.3	510	1	PIA1 HUMAN
6	222	40.8	507	1	PIA2 HUMAN
7	92.5	17.0	726	1	PIA1 MOUSE
8	88.5	16.3	627	1	PIA1 XENLA
9	76	14.0	1479	1	BA1B MOUSE
10	74.5	13.7	1025	1	CE2 MOUSE
11	73.5	13.5	765	1	PIA1 MOUSE
12	72.5	13.3	469	1	CHBP MOUSE
13	72	13.2	129	1	YN70 ARCFU
14	69.5	12.8	249	1	PIA1 ARATH
15	69.5	12.8	250	1	EX11 ARATH
16	69.5	12.8	269	1	EX23 ARATH
17	69.5	12.8	1436	1	WC11 BOVIN
18	68.5	12.6	248	1	EX15 ARATH
19	68	12.5	1556	1	BA1A HUMAN
20	67.5	12.4	92	1	PERN AZOVI
21	67.5	12.4	276	1	EX25 ARATH
22	67.5	12.4	462	1	MSTA DROME
23	67.5	12.4	661	1	HT31 ARATH
24	67	12.3	230	1	YF42 METKA
25	67	12.3	235	1	Y057 CAEEL
26	67	12.3	1453	1	CA11 CHICK
27	66.5	12.2	768	1	ITB8 RABIT
28	66	12.1	332	1	TRPD VIBPA
29	66	12.1	526	1	HRG RABIT
30	66	12.1	1972	1	BA2B HUMAN
31	65	11.9	331	1	TRPD CLOAB
32	65	11.9	851	1	CT06 HUMAN
33	65	11.9	1483	1	BA1B HUMAN

34	65	11.9	1516	1	CALH HUMAN
35	65	11.9	3565	1	CSM1 HUMAN
36	64.5	11.9	101	1	FER PYRIS
37	64.5	11.9	124	1	RS16 RHIME
38	64.5	11.9	5038	1	RYR1 HUMAN
39	63.5	11.7	260	1	EX16 ARATH
40	63.5	11.7	473	1	MDM2 XENLA
41	63	11.6	246	1	TLPI PRUPE
42	63	11.6	662	1	DCHS MOUSE
43	63	11.6	877	1	PI01 PIG
44	63	11.6	1235	1	RNT1 ARATH
45	62.5	11.5	258	1	EXP9 ARATH

ALIGNMENTS

RESULT 1
PIA3_HUMAN STANDARD; PRT; 619 AA.
AC Q9Y6X2; Q9UF13;
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Protein inhibitor of activated STAT protein 3.
GN PIA33
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=9233144; PubMed=10319586;
RA Ueki N., Seki N., Yano K., Saito T., Masuho Y., Muramatsu M.;
RT "Isolation and chromosomal assignment of a human gene encoding protein
inhibitor of activated STAT3 (PIA33).";
RL J. Hum. Genet. 44:193-196(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood, and Muscle;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Gough J., Schmutz J., Myers R.M.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [3]
RP SEQUENCE OF 301-619 FROM N.A.
RC TISSUE=Breast cancer;
RA Poustka A., Klein M., Mewes H.-W., Gassenhuber J., Wiemann S.;
Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Specifically inhibits activated STAT3 signaling by
blocking its DNA-binding activity.
CC -!- SUBCELLULAR LOCATION: Nuclear (By similarity).
CC -!- TISSUE SPECIFICITY: Widely expressed.
CC -!- SIMILARITY: Contains 1 SAP domain.
CC -!- SIMILARITY: Contains 1 MIZ-type zinc finger.

P39060	homo sapien
Q96P27	homo sapien
P81901	thyroaculum m
Q92143	rhizobium m
P21817	homo sapien
Q9M289	arabidopsis
P56273	xenopus lae
P83332	prunus pers
P23738	mus musculus
O02696	sus scrofa
Q9FJ00	arabidopsis
Q91299	arabidopsis

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DR EMBL; AB021868; BAA78533.1; --
DR EMBL; BC001154; AAH01154.1; --
DR EMBL; BC030556; AAH30556.1; --
DR EMBL; AL122061; CAB59241.1; --
DR PIR; T34525; T34525.
DR MIM; 605987; --
DR InterPro; IPR003034; SAP.
DR InterPro; IPR004181; Znf_MIZ.
DR Pfam; PF02037; SAP; 1.
DR Pfam; PF02891; zf-MIZ; 1.
DR SMART; SM00513; SAP; 1.
DR PROSITE; PS00800; SAP; 1.
KW Zinc-finger; Nuclear protein.
FT DOMAIN 2 36
FT ZN_FING 314 366 MIZ-TYPE.
SQ SEQUENCE 619 AA; 67008 MW; A749A877D8925AC7 CRC64;

Query Match 100.0%; Score 544; DB 1; Length 619;
Best Local Similarity 100.0%; Pred. No. 1.3e-48;
Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TWTCPVCDKAPYESLIIDGLFMEILSSCSDCDEIQFMEDGWCMPKPKKEASEVCPPPG 60
DB 354 TWTCPVCDKAPYESLIIDGLFMEILSSCSDCDEIQFMEDGWCMPKPKKEASEVCPPPG 413
QY 61 YGLDGLQYSPVGGDPSENKKKVEVDLTIESSSDEEDL 99
DB 414 YGLDGLQYSPVGGDPSENKKKVEVDLTIESSSDEEDL 452

RESULT 2

PIA3 MOUSE
ID PIA3_MOUSE STANDARD; PRT; 584 AA.
AC 054714;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Protein inhibitor of activated STAT protein 3.
GN PIAS3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98049615; PubMed=9388184;
RA Chung C.D., Liao J., Rao X., Jay P., Berta P., Shuai K.;
RT "Specific inhibition of Stat3 signal transduction by PIAS3.";
RL Science 278:1803-1805 (1997).
CC -1- FUNCTION: Specifically inhibits activated STAT3 signaling by
CC blocking its DNA-binding activity.
CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).
CC -1- SIMILARITY: Contains 1 SAP domain.
CC -1- SIMILARITY: Contains 1 MIZ-type zinc finger.

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DR EMBL; AF034080; AAB88902.2; --
DR MGD; MGI:1913126; Pias3.

DR InterPro; IPR003034; SAP.
DR InterPro; IPR004181; Znf_MIZ.
DR Pfam; PF02037; SAP; 1.
DR Pfam; PF02891; zf-MIZ; 1.
DR SMART; SM00513; SAP; 1.
DR PROSITE; PS00800; SAP; 1.
KW Zinc-finger; Nuclear protein.
FT DOMAIN 2 36
FT ZN_FING 279 331 MIZ-TYPE.
SQ SEQUENCE 584 AA; 63652 MW; 8567831ACALD0D98 CRC64;

Query Match 91.0%; Score 495; DB 1; Length 584;
Best Local Similarity 91.9%; Pred. No. 1.4e-43;
Matches 91; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 TWTCPVCDKAPYESLIIDGLFMEILSSCSDCDEIQFMEDGWCMPKPKKEASEVCPPPG 60
DB 319 TWTCPVCDKAPYESLIIDGLFMEILSSCSDCDEIQFMEDGWCMPKPKKEASEVCPPPG 378
QY 61 YGLDGLQYSPVGGDPSENKKKVEVDLTIESSSDEEDL 99
DB 379 YGLDGLQYSPVGGDPSENKKKVEVDLTIESSSDEEDL 417

RESULT 3

PIA1 MOUSE
ID PIA1_MOUSE STANDARD; PRT; 651 AA.
AC 088007;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Protein inhibitor of activated STAT protein 1 (DEAD/H box binding
DE protein 1).
GN PIAS1 OR DDBP1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=B-cell;
RX MEDLINE=98393695; PubMed=9724754;
RA Liu B., Liao J., Rao X., Mushner S.A., Chung C.D., Chang D.D.,
RA Shuai K.;
RT "Inhibition of Stat1-mediated gene activation by PIAS1.";
RL Proc. Natl. Acad. Sci. U.S.A. 96:10626-10631 (1998).
CC -1- FUNCTION: Specifically inhibits activated STAT1 signaling by
CC blocking its DNA-binding activity.
CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).
CC -1- SIMILARITY: Contains 1 SAP domain.
CC -1- SIMILARITY: Contains 1 MIZ-type zinc finger.

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DR EMBL; AF077950; AAC36701.1; --
DR MGD; MGI:1913125; Pias1.
DR InterPro; IPR003034; SAP.
DR InterPro; IPR004181; Znf_MIZ.
DR Pfam; PF02037; SAP; 1.
DR Pfam; PF02891; zf-MIZ; 1.
DR SMART; SM00513; SAP; 1.
DR PROSITE; PS00800; SAP; 1.
KW Repeat; Zinc-finger; Nuclear protein.
FT DOMAIN 11 45
FT ZN_FING 331 383 MIZ-TYPE.
FT DOMAIN 56 64 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
FT DOMAIN 368 380 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 25, 2004, 01:30:24 ; Search time 14.754 Seconds
(without alignments)
2018.720 Million cell updates/sec

Title: US-10-075-074-6

Perfect score: 2943

Sequence: 1 MKIKLYRRFRFKTLGPSD.....GPLPSPGLTGRSDIXSLD 572

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2816	95.7	619	1 PIA3_HUMAN	Q9y6x2 homo sapien
2	2573.5	87.4	584	1 PIA3_MOUSE	O54714 mus musculus
3	1488.5	50.6	651	1 PIA1_MOUSE	O88907 mus musculus
4	1480.5	50.3	651	1 PIA1_HUMAN	O75925 mus sapien
5	893	30.3	510	1 PIA2_HUMAN	Q9n2w9 homo sapien
6	881.5	30.0	507	1 PIA2_MOUSE	Q9jmo5 mus musculus
7	204	6.9	726	1 NF11_YEAST	Q12216 saccharomyc
8	141	4.8	1509	1 GSR1_HUMAN	Q9nzm4 homo sapien
9	130.5	4.4	1329	1 KP10_HUMAN	Q9p218 homo sapien
10	120	4.1	893	1 DAL1_MOUSE	Q62165 mus musculus
11	119.5	4.1	1088	1 MPTB_HUMAN	Q9ulh7 homo sapien
12	119	4.0	1300	1 SAL3_HUMAN	Q9bxa9 homo sapien
13	118	4.0	895	1 DAL1_BOVIN	O18738 bos taurus
14	118	4.0	895	1 DAL1_HUMAN	Q14118 homo sapien
15	117	4.0	1567	1 FPN2_MOUSE	Q9j104 mus musculus
16	116.5	4.0	1257	1 PCGN_RAT	P55067 rattus norv
17	116	3.9	2063	1 NCO6_HUMAN	Q14686 h nuclear r
18	115	3.9	487	1 BEN2_EBV	P12978 Epstein-bar
19	114.5	3.9	1072	1 MAP4_BOVIN	P36225 bos taurus
20	113.5	3.9	542	1 ZYX_CHICK	O04584 gallus gall
21	113.5	3.9	1574	1 SYJ1_RAT	Q02910 rattus norv
22	113	3.8	5262	1 ML12_HUMAN	O14686 homo sapien
23	112	3.8	2364	1 PCGN_BOVIN	P13608 bos taurus
24	112	3.8	3866	1 HRX_MOUSE	P55200 mus musculus
25	111	3.8	3164	1 TEGU_HSV1	P10220 herpes simp
26	110.5	3.8	852	1 WS14_HUMAN	Q9np71 homo sapien
27	110	3.7	895	1 DAL1_RABIT	O28685 oryctolagus
28	110	3.7	1515	1 CALH_HUMAN	P39060 homo sapien
29	109.5	3.7	1003	1 MBD6_HUMAN	Q96dnc homo sapien
30	109.5	3.7	1142	1 KPCI_NEUCR	P87253 neurospora
31	108.5	3.7	789	1 ATX1_RAT	Q63540 rattus norv
32	108.5	3.7	901	1 A180_MOUSE	Q61548 mus musculus
33	108.5	3.7	5179	1 MDC2_HUMAN	Q02817 homo sapien

ALIGNMENTS

RESULT 1
PIA3_HUMAN
ID PIA3_HUMAN STANDARD; PRT; 619 AA.
AC Q9Y6X2; Q9UFI3;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Protein inhibitor of activated STAT protein 3.
GN PIA33.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=9253144; PubMed=10319586;
RA Ueki N., Seki N., Yano K., Saito T., Masuho Y., Muramatsu M.;
RT "Isolation and chromosomal assignment of a human gene encoding protein
inhibitor of activated STAT3 (PIA33).";
RL J. Hum. Genet. 44:193-196(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood, and Muscle;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Schmerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [3]
RP SEQUENCE OF 301-619 FROM N.A.
RC TISSUE=Breast cancer;
RA Poustka A., Klein M., Mewes H.-W., Gassenhuber J., Wiemann S.;
Submitted (Oct-1999) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Specifically inhibits activated STAT3 signaling by
blocking its DNA-binding activity.
CC -!- SUBCELLULAR LOCATION: Nuclear [by similarity].
CC -!- TISSUE SPECIFICITY: Widely expressed.
CC -!- SIMILARITY: Contains 1 SAP domain.
CC -!- SIMILARITY: Contains 1 MTZ-type zinc finger.

34 108.5 3.7 5703 1 MUSB_HUMAN Q9hc84 homo sapien
35 107 3.6 1152 1 MAP4_HUMAN P27816 homo sapien
36 107 3.6 1324 1 IRS2_HUMAN Q9y4h2 homo sapien
37 107 3.6 5038 1 PCLO_MOUSE Q9gyx7 mus musculus
38 107 3.6 5147 1 PCLO_HUMAN Q9y6v0 homo sapien
39 106.5 3.6 1812 1 BRC1_MOUSE P48754 mus musculus
40 106 3.6 634 1 Z297_HUMAN O15209 homo sapien
41 106 3.6 639 1 SF01_HUMAN Q15637 homo sapien
42 106 3.6 3859 1 TRAP_HUMAN Q9y4a5 homo sapien
43 105.5 3.6 1321 1 IRS2_MOUSE P81122 mus musculus
44 105.5 3.6 1822 1 ZAP3_HUMAN P49750 homo sapien
45 105 3.6 936 1 MRTA_XENLA Q8ayc2 xenopus lae

371 SEVCPGKGLDQYSAVQGIQESKREVEIDLTIESSEDEDLPTTKKHCPTVSA 430
 420 IPALPGSKGLTSGHQSSVLRSPAMGTGKXDFLSSLPHEYPAPPLGADIQGLDLFSF 479
 431 IPALPGSKGALTSGHQSSVLRSPAMGTGKXDFLSSLPHEYPAPPLGADIQGLDLFSF 490
 480 LQTES-QYXPSVITSLDEQXGLGHFFQXRTTPKHFLGFLAPTGLGSSXSATPAPXGVRV 538
 491 LQTESQYGFSEVITSLDEQXGLGHFFQXRTTPKHFLGFLAPTGLGSSXSATPAPXGVRV 550
 539 SIVAPGXXLREGHGGLPSPGSLTGCRSDIXSLD 572
 551 SIVAPGSSSLREGHGGLPSPGSLTGCRSDVSLD 584

RESULT 3
 ID PIAL MOUSE STANDARD; PRT; 651 AA.
 AC 088907;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DE Protein inhibitor of activated STAT protein 1 (DEAD/H box binding protein 1).
 GN PIA1 OR DDXBP1.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RC SEQUENCE FROM N.A.
 RX TISSUE=B-cell;
 RA Liu B., Liao J., Rao X., Kushner S.A., Chung C.D., Chang D.D., Shuai K.;
 RT "Inhibition of Stat1-mediated gene activation by PIA1.";
 RL Proc. Natl. Acad. Sci. U.S.A. 95:10626-10631(1998).
 CC -1- FUNCTION: Specifically inhibits activated STAT1 signaling by blocking its DNA-binding activity.
 CC -1- SUBCELLULAR LOCATION: Nuclear (by similarity).
 CC -1- SIMILARITY: Contains 1 SAP domain.
 CC -1- SIMILARITY: Contains 1 MIZ-type zinc finger.
 CC
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 CC
 CC EMBL; AF077950; AAC36701.1; -
 CC MGD; MGI:1913125; Pias1.
 CC InterPro; IPR003034; SAP.
 CC InterPro; IPR004181; Znf_MIZ.
 CC Pfam; PF02037; SAP; 1.
 CC Pfam; PF02891; zf-MIZ; 1.
 CC SMART; SM00513; SAP; 1.
 CC PROSITE; PS00800; SAP; 1.
 CC Repeat; Zinc-finger; Nuclear protein.
 CC FT DOMAIN 11 45
 CC FT ZN_FING 331 383
 CC FT DOMAIN 56 64
 CC FT DOMAIN 368 380
 CC FT DOMAIN 577 634
 CC FT DOMAIN 520 615
 CC FT REPEAT 520 523
 CC FT REPEAT 557 560
 CC FT REPEAT 598 601
 CC FT REPEAT 612 615
 CC SEQUENCE 651 AA; 71607 MW; DBD544128E817C81 CRC64;
 SQ
 Query Match 50.6%; Score 1488.5; DB 1; Length 651;

Best Local Similarity 53.6%; Pred. No. 3.4e-100;
 Matches 329; Conservative 74; Mismatches 152; Indels 59; Gaps 19;
 1 MKIKELYRRRPPKRTIGPSDLSLLSPGGTSPVGSXPALXIPPTL-----L 47
 55 MKIKELYRRRFPQKINTPADLSIPNVH-----SSMPPTLSPSTIPQLTIDYGHGHPASSPL 108
 48 XPCITLGPKEVDMDHPLP---OPVHPDVTMKLPFVGVGELIRPTTTLASTSSQRFEEA 104
 109 LPVSLGLGRHELSL-PHLTSALHPVHPDIKQLPFYDLDDELIKPTSLASDMSQRFRET 167
 105 HFTFALTPOQXQOILTSREVLPGAKLDYTIQVLRFLCETSLPQEDYFPNLFVKVNGK 164
 168 CFALFALTPOQVQOISSMDI-SGTKCDFTVQVQLRFLCETSCPQEDHFPNLCVKVNTK 226
 165 LCPILGYLPPTKNGAEPKRSRINITPKARLSATVPNTIVVWSSSEFGNTSLSVLVR 224
 227 PCSLPGLYLPPTKNGVEPKRSRINITSLVRLSTTVNTIVWSWTAEIGRTYSMAVYLK 286
 225 QLTAGTLQKLRAGIRNPDHRSALIKGLTADPDGVAATTSRVSMLCPLGKRLTVPC 284
 287 QLSSTVLLQRLRAGIRNPDHRSALIKGLTADSDSEIATTSRVSLLCPLGKRLTIPC 346
 285 RALTCAHLQSFSAALYLQMNE-KPTWTCTPCVCDKAPWESLIIDGLFMEILKXSCDCDEIQ 343
 347 RALTCSHLQCFDALTLYIQMNEKPTWVCPVCDKAPVEHLIIDGLFMEILKYCTDCDEIQ 406
 344 FMEDGSTCCKPKKAEASEVCPFGY-GLDG-----LQYSPVQXGXPSENKKXVEVIDLTI 397
 407 FKEDGSAWAPMRSKVEQEV--TASYNGVDGCLSTLEHVAHQSSNNKKKVEVIDLTI 464
 398 ESSSD-EEDLPPTPKKCKVTSAAIPALPGSKGLTSGHQSSVLRSPAMGTGLGKDFLSSL 456
 465 DSSDEEEEPKAKRTCPSPISPL--SNKGILSLPHQSPVSRTPSLPAVDTSYNTS 522
 457 PLHEYPPAF---PLGADIQGLDLFSFLQTESQ-YXPSVITSL-----DEQXGLGHFFQXR 507
 523 LIQDYRHPFHMTMPYDLOGLDREPFSLGDNQHVNTSLAAAVASDDQDLL---HSSR 579
 508 FTP-----XHFGLPLAPTLGSHXSNATPAPXGVRVSSIVAPGXLLREGHGGLPSP-----G 558
 580 FFPYTSSQMFLDQLSAG-GSTSLPATNGSSSGSSNLSVLS-SNLSRSHGHGVASRSSADT 637
 559 PSLTGCRSDIXSLD 572
 638 ASIFGIIPDIISLD 651

RESULT 4
 ID PIAL HUMAN STANDARD; PRT; 651 AA.
 AC O75925; Q99751; Q9UN02;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DE Protein inhibitor of activated STAT protein 1 (Gu binding protein) (GBP) (RNA helicase II binding protein) (DEAD/H box-binding protein 1).
 GN PIA1 OR DDXBP1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RC SEQUENCE FROM N.A., AND FUNCTION.
 RC TISSUE=B-cell;
 RX MEDLINE=98393695; PubMed=9724754;
 RA Liu B., Liao J., Rao X., Kushner S.A., Chung C.D., Chang D.D., Shuai K.;
 RT "Inhibition of Stat1-mediated gene activation by PIA1.";
 RL Proc. Natl. Acad. Sci. U.S.A. 95:10626-10631(1998).
 RN [2]
 RP SEQUENCE FROM N.A.

RX MEDLINE=20092325; PubMed=10628744;
 RA Tan J., Hall S.H., Hamil K.G., Grossman G., Petrusz P., Liao J.,
 RA Shuai K., French P.S.,
 RT "protein inhibitor of activated STAT-1 (signal transducer and
 RT activator of transcription-1) is a nuclear receptor coregulator
 RT expressed in human testis.";
 RL Mol. Endocrinol. 14:14-26(2000).
 RN [3]
 RP SEQUENCE OF 7-650 FROM N.A., SUBCELLULAR LOCATION, AND TISSUE
 RP SPECIFICITY.
 RC TISSUE=B-cell;
 RX MEDLINE=97320420; PubMed=9177271;
 RA Valdez B.C., Henning D., Perlaky L., Busch R.K., Busch H.;
 RT "Cloning and characterization of Gu/RH-II binding protein.";
 RL Biochem. Biophys. Res. Commun. 234:335-340(1997).
 CC -!- FUNCTION: Specifically inhibits activated STAT1 signaling by
 CC blocking its DNA-binding activity.
 CC -!- SUBUNIT: Binds p53, RNA helicase-II and androgen receptor.
 CC -!- SUBCELLULAR LOCATION: Nuclear.
 CC -!- TISSUE SPECIFICITY: Highly expressed in testis.
 CC -!- SIMILARITY: Contains 1 SAP domain.
 CC -!- SIMILARITY: Contains 1 MIZ-type zinc finger.
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; AF077951; AAC36702.1; -;
 DR EMBL; AF167160; AAD49722.1; -;
 DR EMBL; U78524; AAB58488.1; -;
 DR Genew; HGNC:2752; PIAS1.
 DR MIM; 603566; -;
 DR GO; GO:0005634; C:nucleus; TAS.
 DR GO; GO:0003714; F:transcription co-repressor activity; TAS.
 DR GO; GO:0007259; P:JAK-STAT cascade; TAS.
 DR InterPro; IPR003034; SAP.
 DR InterPro; IPR004181; ZnF_MIZ.
 DR Pfam; PF02037; SAP; 1.
 DR Pfam; PF02891; zf-Miz; 1.
 DR SMART; SM00513; SAP; 1.
 DR PROSITE; PS00800; SAP; 1.
 DR Repeat; Zinc-finger; Nuclear protein.
 FT DOMAIN 11 45
 FT SAP.
 FT ZN_FING 331 383
 FT MIZ-TYPE.
 FT NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
 FT NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
 FT SER-RICH.
 FT 4 X 4 AA REPEATS OF N-T-S-L.
 FT 1.
 FT 2.
 FT 3 (APPROXIMATE).
 FT 4 (APPROXIMATE).
 FT E -> K (IN REF. 1).
 FT IVV -> MC (IN REF. 1).
 FT S -> T (IN REF. 3).
 FT SEQUENCE 651 AA; 71835 MW; AA69338221124119 CRC64;

Query Match 50.3%; Score 1480.5; DB 1; Length 651;
 Best Local Similarity 53.1%; Pred. No. 1.3e-99;
 Matches 326; Conservative 77; Mismatches 152; Indels 59; Gaps 19;
 QY 1 MKIKELVRRPRKTLGSDLSLSLPGTSPVSGSPXAPIPTL-----L 47
 DB 55 MKIKELVRRPRKTLGSDLSLSLPGTSPVSGSPXAPIPTL-----L 47
 QY 48 XPGTLGPKRVDVHPPLP---QVHPDVTMKPLPFYEVYGEIIRPTTLASTSSORFEA 104
 DB 109 LPVSLGLPKHELEL-PLHTLSALHPVHPDVKLQKLPFYDLDELKPLSLASDNRFRFET 167

QY 105 HTEFALTPOOXOOILTSREVLPAGAKLDYTIQVOLFCLCETSLPOEDYFPNLPFKVXCK 164
 DB 168 CFAPALTPOOXOOISSMDI-SGTKCDFTVQVQRFCLSETSCPOEDHPPNLPKVKNTK 226
 QY 165 LCPFLPGYLPPTKNGAEPKRPSPRINITPKARLSATVPNTIVVMSSSEGRNTSLSVILVR 224
 DB 227 PCSLPGYLPPTKNGVEPKRSPRINITSLVRLSTVPTIVVSWTAELGRNYSMAVYLK 286
 QY 225 QLTAGTLQKLRAKIRNPDHSHRALIKGLTADPDGVAATSLRVSMLCPGLKMLTVPC 284
 DB 287 QLSSTVLLQRLRAKIRNPDHSHRALIKGLTADPDSEIATSLRVSLLCPGLKMLTIPC 346
 QY 285 RALTCALHQSFAALYLQWNE-KPWTCPCVCKKAPMESLIIDGLFMEILKSCSDCDRIQ 343
 DB 347 RALTCHLQCDATLIYQMKERKPTWPCVCKKAPYBHLIIDGLFMEILKYCTDCDBIQ 406
 QY 344 FMEDGSTCPMKPKKEASVCPGGY-GLDG-----LOYSPVQXGXPSNKXKVEVIDLTI 397
 DB 407 FKEDGTWAPMSKKEVQEV--SASVNGVDGCLSLTEHQVASHHQSNNKKNKVEVIDLTI 464
 QY 398 ESSSDEBOLPPT-KHCHVTSAAIPALPGSKGLTSGHOPSVLRSVPAMGTIGXDFLSL 456
 DB 465 DSSDEEERPSAKRTCSLSTPSL--NNKGILSLPHQASPVSKRTPSLPAVDTSYINTS 522
 QY 457 PLHEVPPAF---PLGADIQGLDLFSFLQTESQ-YKXPSVITSL-----DEQDXLGHFFQXR 507
 DB 523 LIQYRHPFHTMPYDQLQGLDFFFLSGDNQHNYSLLAAAAVSDQDL-----HSSR 579
 QY 508 FTP---XHFGLPLAPTIGSSHXSATPAPXPRGVSSIVAPGXLLREGHGGLPS-----G 558
 DB 580 FFPVTSSQMFLDQLSAG-GSTSLPTNGSSGSSSLVS-SNSLRESHSHVTNRSSDT 637
 QY 559 PSLTGCSDIXSLD 572
 DB 638 ASIFGIIPDIISLD 651
 RESULT 5
 ID PIAG HUMAN STANDARD; PRT; 510 AA.
 AC Q8N2W9; O75926; Q96G19; Q9UN16;
 DT 10-OCT-2003 (Rel. 42, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Protein inhibitor of activated STAT protein gamma (PIAS-gamma)
 DE (PIASγ).
 GN PIASG.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=B-cell;
 RX MEDLINE=98393695; PubMed=9724754;
 RA Liu B., Liao J., Rao X., Kushner S.A., Chung C.D., Chang D.D.,
 RA Shuai K.;
 RT "Inhibition of Stat1-mediated gene activation by PIAS1.";
 RL Proc. Natl. Acad. Sci. U.S.A. 95:10626-10631(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain, Lung, and Skin;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan M., Moore T., Max S.I., Wang J.M., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

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OM protein - protein search, using sw model

Run on: August 25, 2004, 01:30:24 ; Search time 2.55357 Seconds
(without alignments)
2018.720 Million cell updates/sec

Title: US-10-075-074-7

Perfect score: 543

Sequence: 1 TWTCPCVCKKAPYSLIIDG.....KKRVEVDLTIESSSDEEDL 99

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	517	95.2	619	PIA3_HUMAN	Q9y6x2 homo sapien
2	516	95.0	584	PIA3_MOUSE	Q54714 mus musculus
3	332	61.1	651	PIA1_MOUSE	O88907 mus musculus
4	324	59.7	651	PIA1_HUMAN	O75925 homo sapien
5	251.5	46.3	510	PIA2_HUMAN	Q8n2w9 homo sapien
6	218	40.1	507	PIA2_MOUSE	Q9jrm05 mus musculus
7	95	17.5	726	PIA1_YEAST	Q12216 saccharomyc
8	91.5	16.9	627	BA1A_XENLA	Q8uvz5 xenopus lae
9	79.5	14.6	469	C4BP_MOUSE	P08607 mus musculus
10	76.5	14.1	462	MSTA_DROME	O46040 drosophila
11	75	13.8	1556	BA1A_HUMAN	Q9nr12 h bromodoma
12	74	13.6	1479	BA1B_MOUSE	Q9z277 mus musculus
13	72.5	13.4	765	PF10_MOUSE	Q923p0 mus musculus
14	72	13.3	651	YIRF_SCHPO	Q9p713 schizosacch
15	71	13.1	129	YN70_ARCFU	O30300 archaeoglob
16	70.5	13.0	269	EX23_ARATH	Q9fl79 arabidopsis
17	70.5	13.0	1025	CR2_MOUSE	P19070 mus musculus
18	69.5	12.8	249	EX10_ARATH	Q9ldr9 arabidopsis
19	69.5	12.8	250	EX01_ARATH	Q9c554 arabidopsis
20	69.5	12.8	881	PHFE_MOUSE	Q9d4h9 mus musculus
21	68.5	12.6	248	EX15_ARATH	O80622 arabidopsis
22	68.5	12.6	276	EX25_ARATH	Q9fl77 arabidopsis
23	68.5	12.6	661	HT31_ARATH	Q04996 arabidopsis
24	67	12.3	888	PHFE_HUMAN	Q94880 homo sapien
25	65.5	12.1	101	FER_PYRIS	P19101 pyrobaculum
26	65.5	12.1	5038	RYR1_HUMAN	P21817 homo sapien
27	65	12.0	335	FAH1_BACTN	Q8ab18 bacteroides
28	65	12.0	5037	RYR1_RABIT	P11716 oryctolagus
29	64.5	11.9	92	FERN_AZOFI	P11054 azotobacter
30	64.5	11.9	1483	BA1B_HUMAN	Q9u190 homo sapien
31	64	11.8	538	RB55_HUMAN	Q15291 homo sapien
32	64	11.8	1227	PR16_HUMAN	Q92620 homo sapien
33	64	11.8	3565	CSM1_HUMAN	Q96pz7 homo sapien

34	63.5	11.7	260	1	EX16_ARATH	Q9m2s9 arabidopsis
35	63	11.6	519	1	IKAR_HUMAN	Q13422 homo sapien
36	63	11.6	543	1	SUW2_HUMAN	Q86yh2 homo sapien
37	63	11.6	877	1	PI01_PIG	O02696 sus scrofa
38	63	11.6	1173	1	TSPI_XENLA	P35448 xenopus lae
39	63	11.6	4911	1	MLL3_HUMAN	Q91z99 arabidopsis
40	62.5	11.5	258	1	EXP3_ARATH	O80932 arabidopsis
41	62.5	11.5	262	1	EXP3_ARATH	O80932 arabidopsis
42	62.5	11.5	291	1	ZUP1_CAMJE	Q9pin2 campylobact
43	62.5	11.5	303	1	ATNB_CANFA	P06583 canis famill
44	62.5	11.5	326	1	PDL1_MOUSE	O70400 mus musculu
45	62.5	11.5	731	1	CND2_MOUSE	Q8c156 mus musculu

ALIGNMENTS

RESULT 1
PIA3_HUMAN STANDARD; PRT; 619 AA.
AC Q9Y6X2; Q9YF13;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Protein inhibitor of activated STAT protein 3.
GN PIA33
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99253144; PubMed=10319586;
RA Ueki N., Seki N., Yano K., Saito I., Masuho Y., Muramatsu M.;
RT Isolation and chromosomal assignment of a human gene encoding protein
inhibitor of activated STAT3 (PIA33).";
J. Hum. Genet. 44:193-196(1999).
[2]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood, and Muscle;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L.H., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan K., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.W., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Fahey J., Helton E., Kettelman M., Maman A., Rodriguez S., Sanchez A.,
Whiting M., Maman A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Schnurch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT *Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[3]
RP SEQUENCE OF 301-619 FROM N.A.
RC TISSUE=Breast cancer;
RA Poustka A., Klein M., Mewes H.-W., Gassenhuber J., Wiemann S.;
Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
RL Poustka A., Klein M., Mewes H.-W., Gassenhuber J., Wiemann S.;
Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Specifically inhibits activated STAT3 signaling by
blocking its DNA-binding activity.
CC -!- SUBCELLULAR LOCATION: Nuclear (By similarity).
CC -!- TISSUE SPECIFICITY: Widely expressed.
CC -!- SIMILARITY: Contains 1 SAP domain.
CC -!- SIMILARITY: Contains 1 MIZ-type zinc finger.

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EMBL; AB021869; BAA78533.1; -
 EMBL; BC001154; AAH01154.1; -
 EMBL; BC030556; AAH030556.1; -
 EMBL; AL122061; CAB59241.1; -
 PIR; T34525; T34525.
 MIM; 605987; -
 InterPro; IPR003034; SAP.
 InterPro; IPR004181; Znf_MIZ.
 Pfam; PF02037; SAP; 1.
 Pfam; PF02891; zf-MIZ; 1.
 SMART; SM00513; SAP; 1.
 PROSITE; PS50800; SAP; 1.
 Zinc-finger; Nuclear protein.
 DOMAIN 2 36
 ZN_FING 314 366 MIZ-TYPE.
 FT SEQUENCE 619 AA; 67008 MW; A749A877D8925AC7 CRC64;

Query Match 95.2%; Score 517; DB 1; Length 619;
 Best Local Similarity 94.9%; Pred. No. 3.6e-46;
 Matches 94; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 TWTCPVCDKAPYESLIIDGLFMEILNSCSDCEIQFMEDGSCWCPMKPKKEASEVCPPPG 60
 DB 354 TWTCPVCDKAPYESLIIDGLFMEILNSCSDCEIQFMEDGSCWCPMKPKKEASEVCPPPG 413

QY 61 YGLDGLQYSPVQEGNQSENKKRVEVDLTIESSSDEEDL 99
 DB 414 YGLDGLQYSPVQEGNQSENKKRVEVDLTIESSSDEEDL 452

RESULT 2

PIA3_MOUSE
 ID PIA3_MOUSE STANDARD; PRT; 584 AA.
 AC 054714;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Protein inhibitor of activated STAT protein 3.
 GN PIAS3.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98049615; PubMed=9388184;
 RA Chung C.D., Liao J., Rao X., Jay P., Berta P., Shuai K.;
 RT Specific inhibition of Stat3 signal transduction by PIAS3.;
 RL Science 278:1803-1805 (1997).
 CC -!- FUNCTION: Specifically inhibits activated STAT3 signaling by
 CC blocking its DNA-binding activity.
 CC -!- SUBCELLULAR LOCATION: Nuclear (By similarity).
 CC -!- SIMILARITY: Contains 1 SAP domain.
 CC -!- SIMILARITY: Contains 1 MIZ-type zinc finger.

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EMBL; AF034080; AAB88902.2; -
 MGD; MGI:1913126; Pias3.

DR InterPro; IPR003034; SAP.
 DR InterPro; IPR004181; Znf_MIZ.
 DR Pfam; PF02037; SAP; 1.
 DR Pfam; PF02891; zf-MIZ; 1.
 DR SMART; SM00513; SAP; 1.
 DR PROSITE; PS50800; SAP; 1.
 KW Zinc-finger; Nuclear protein.
 FT DOMAIN 2 36
 ZN_FING 279 331 MIZ-TYPE.
 SQ SEQUENCE 584 AA; 63652 MW; 8567831ACALD0D98 CRC64;

Query Match 95.0%; Score 516; DB 1; Length 584;
 Best Local Similarity 96.0%; Pred. No. 4.3e-46;
 Matches 95; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 TWTCPVCDKAPYESLIIDGLFMEILNSCSDCEIQFMEDGSCWCPMKPKKEASEVCPPPG 60
 DB 319 TWTCPVCDKAPYESLIIDGLFMEILNSCSDCEIQFMEDGSCWCPMKPKKEASEVCPPPG 378

QY 61 YGLDGLQYSPVQEGNQSENKKRVEVDLTIESSSDEEDL 99
 DB 379 YGLDGLQYSPVQEGNQSENKKRVEVDLTIESSSDEEDL 417

RESULT 3

PIA1_MOUSE
 ID PIA1_MOUSE STANDARD; PRT; 651 AA.
 AC 089907;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Protein inhibitor of activated STAT protein 1 (DEAD/H box binding
 DE protein 1).
 GN PIAS1 OR DDX41.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=B-Cell;
 RX MEDLINE=98393695; PubMed=9724754;
 RA Liu B., Liao J., Rao X., Kashner S.A., Chung C.D., Chang D.D.,
 RA Shuai K.;
 RT Inhibition of Stat1-mediated gene activation by PIAS1.;
 RL Proc. Natl. Acad. Sci. U.S.A. 95:10626-10631 (1998).
 CC -!- FUNCTION: Specifically inhibits activated STAT1 signaling by
 CC blocking its DNA-binding activity.
 CC -!- SUBCELLULAR LOCATION: Nuclear (By similarity).
 CC -!- SIMILARITY: Contains 1 SAP domain.
 CC -!- SIMILARITY: Contains 1 MIZ-type zinc finger.

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EMBL; AF077950; AAC36701.1; -
 MGD; MGI:1913125; Pias1.
 DR InterPro; IPR003034; SAP.
 DR InterPro; IPR004181; Znf_MIZ.
 DR Pfam; PF02037; SAP; 1.
 DR Pfam; PF02891; zf-MIZ; 1.
 DR SMART; SM00513; SAP; 1.
 DR PROSITE; PS50800; SAP; 1.
 KW Repeat; Zinc-finger; Nuclear protein.
 FT DOMAIN 11 45
 ZN_FING 331 383 MIZ-TYPE.
 FT DOMAIN 56 64
 FT DOMAIN 368 380 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
 FT DOMAIN 368 380 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).

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OM protein - protein search, using sw model

Run on: August 25, 2004, 01:30:24 ; Search time 2.52778 Seconds
(without alignments)
2018.720 Million cell updates/sec

Title: US-10-075-074-10
Perfect score: 517
Sequence: 1 WTCFVCDKAPYSLIDGL.....KKXVEVDLTIESSDDEDL 98

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	505	97.7	619	PIA3 HUMAN	Q9Y6X2 homo sapien
2	478	92.5	584	PIA3 MOUSE	Q54714 mus musculus
3	314	60.7	651	PIA1 MOUSE	O89907 mus musculus
4	309	59.8	651	PIA1 HUMAN	O75925 homo sapien
5	234.5	45.4	510	PIA2 HUMAN	Q82W9 homo sapien
6	214	41.4	507	PIA2 MOUSE	Q9Ym05 mus musculus
7	87.5	16.9	726	NP11 YEAST	Q12216 saccharomyc
8	81.5	15.8	627	BA1A XENLA	Q8UVR5 xenopus lae
9	70	13.5	469	CABP MOUSE	P08607 mus musculus
10	67	13.0	1479	BA1B MOUSE	Q92277 mus musculus
11	66.5	12.9	92	FRN1 AZOVI	P11054 azotobacter
12	65.5	12.7	1436	WC11 BOVIN	P30205 bos taurus
13	65	12.6	538	RB55 HUMAN	Q15291 homo sapien
14	64.5	12.5	249	EX10 ARATH	Q91DR9 arabidopsis
15	64.5	12.5	250	EX11 ARATH	Q9C554 arabidopsis
16	64.5	12.5	269	EX23 ARATH	O91F79 arabidopsis
17	64.5	12.5	765	KE10 MOUSE	Q923P0 mus musculus
18	64	12.4	995	CG1A DROME	Q9NGC3 drosophila
19	64	12.4	1905	TAGB DICDI	P54683 dictyosteli
20	63.5	12.3	248	EX15 ARATH	O80622 arabidopsis
21	63.5	12.3	335	FAH1 BACTN	Q8AB18 bacteroides
22	63.5	12.3	754	ASPH BOVIN	Q28056 bos taurus
23	63	12.2	3565	CSM1 HUMAN	Q96P27 homo sapien
24	62.5	12.1	276	EX25 ARATH	Q9F177 arabidopsis
25	62.5	12.1	661	HT31 ARATH	Q04996 arabidopsis
26	62.5	12.1	1025	CR2 MOUSE	P19070 mus musculus
27	62	12.0	172	PRP2 RAT	P10164 rattus norv
28	61.5	11.9	5038	RYR1 HUMAN	P21817 homo sapien
29	61	11.8	230	YF42 METKA	Q8CV58 methanopyru
30	60.5	11.7	428	SMY3 HUMAN	Q9U7B4 homo sapien
31	60.5	11.7	610	DRTS TOXGO	Q07422 toxoplasma
32	60	11.6	539	CH60 FUSNN	Q8F5X7 fusobacteri
33	60	11.6	591	UN18 CAEEL	P34815 caenorhabdi

ALIGNMENTS

```

RESULT 1
PIA3_HUMAN
ID PIA3_HUMAN STANDARD; PRT; 619 AA.
AC Q9Y6X2; Q9UF13;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Protein inhibitor of activated STAT protein 3.
GN PIAS3
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=9253144; PubMed=10319586;
RT "Isolation and Chromosomal assignment of a human gene encoding protein
inhibitor of activated STAT3 (PIAS3).";
RL J. Hum. Genet. 44:193-196(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood, and Muscle;
RX MEDLINE=22388257; PubMed=12477932;
RX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Fahey J., Heiton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalusz D.E.,
Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [3]
RP SEQUENCE OF 301-619 FROM N.A.
RC TISSUE=Breast cancer;
RX Poustka A., Klein M., Mewes H.-W., Gassenhuber J., Wiemann S.;
Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Specifically inhibits activated STAT3 signaling by
blocking its DNA-binding activity.
CC -!- SUBCELLULAR LOCATION: Nuclear (By similarity).
CC -!- TISSUE SPECIFICITY: Widely expressed.
CC -!- SIMILARITY: Contains 1 SAP domain.
CC -!- SIMILARITY: Contains 1 MIZ-type zinc finger.

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DR EMBL; AB021868; BAA78533.1; -;
 DR EMBL; BC001154; AAH01154.1; -;
 DR EMBL; BC030556; AAH030556.1; -;
 DR EMBL; AL122061; CAB59241.1; -;
 DR PIR; T34525; T34525.
 DR MIM; 605987; -;
 DR InterPro; IPR003034; SAP.
 DR InterPro; IPR004181; Znf_MIZ.
 DR Pfam; PF02037; SAP; 1.
 DR Pfam; PF02891; zf-MIZ; 1.
 DR SMART; SM00513; SAP; 1.
 DR PROSITE; PS50800; SAP; 1.
 KW Zinc-finger; Nuclear protein.
 FT DOMAIN 2 36
 FT ZN_FING 314 366 MIZ-TYPE.
 SQ SEQUENCE 619 AA; 67008 MW; A749A877D8925AC7 CRC64;

Query Match 97.7%; Score 505; DB 1; Length 619;
 Best Local Similarity 94.9%; Pred. No. 1.3e-48;
 Matches 93; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 WTCPCVCDKKAPYESLIIDGLFMEILXSCSDCEIQFMEDGSLWPKPKKEASEVCPPGY 60
 DB 355 WTCPCVCDKKAPYESLIIDGLFMEILXSCSDCEIQFMEDGSLWPKPKKEASEVCPPGY 414

QY 61 GLDGLQYSPVQXGSPENKXKVEVDLTIESSSDEEDL 98
 DB 415 GLDGLQYSPVQXGSPENKXKVEVDLTIESSSDEEDL 452

RESULT 2

PIA3 MOUSE
 ID PIA3_MOUSE STANDARD; PRT; 584 AA.
 AC 054714;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Protein inhibitor of activated STAT protein 3.
 GN PIAS3.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98049615; PubMed=9388184;
 RA Chung C.D., Liao J., Liu B., Rao X., Jay P., Berta P., Shuai K.;
 RT "Specific inhibition of Stat3 signal transduction by PIAS3.";
 RL Science 278:1803-1805 (1997)

CC -!- FUNCTION: Specifically inhibits activated STAT3 signaling by
 CC blocking its DNA-binding activity.
 CC -!- SUBCELLULAR LOCATION: Nuclear (By similarity).
 CC -!- SIMILARITY: Contains 1 SAP domain.
 CC -!- SIMILARITY: Contains 1 MIZ-type zinc finger.

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DR EMBL; AF034080; AAB89902.2; -;
 DR MGD; MGI:1913126; Pias3.

DR InterPro; IPR003034; SAP.
 DR InterPro; IPR004181; Znf_MIZ.
 DR Pfam; PF02037; SAP; 1.
 DR Pfam; PF02891; zf-MIZ; 1.
 DR SMART; SM00513; SAP; 1.
 DR PROSITE; PS50800; SAP; 1.
 KW Zinc-finger; Nuclear protein.
 FT DOMAIN 2 36
 FT ZN_FING 279 331 MIZ-TYPE.
 SQ SEQUENCE 584 AA; 63652 MW; 8567831ACALDOD98 CRC64;

Query Match 92.5%; Score 478; DB 1; Length 584;
 Best Local Similarity 90.8%; Pred. No. 1.3e-45;
 Matches 89; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

QY 1 WTCPCVCDKKAPYESLIIDGLFMEILXSCSDCEIQFMEDGSLWPKPKKEASEVCPPGY 60
 DB 320 WTCPCVCDKKAPYESLIIDGLFMEILXSCSDCEIQFMEDGSLWPKPKKEASEVCPPGY 379

QY 61 GLDGLQYSPVQXGSPENKXKVEVDLTIESSSDEEDL 98
 DB 380 GLDGLQYSAVQGIQFESKRVVVDLTIESSSDEEDL 417

RESULT 3

PIA1 MOUSE
 ID PIA1_MOUSE STANDARD; PRT; 651 AA.
 AC Q88907;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Protein inhibitor of activated STAT protein 1 (DEAD/H box binding
 DE protein 1).
 GN PIAS1 OR NXPB1.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX TISSUE=B-cell;
 RX MEDLINE=98393695; PubMed=9724754;
 RA Liu B., Liao J., Rao X., Kushner S.A., Chung C.D., Chang D.D.,
 RA Shuai K.;
 RT "Inhibition of Stat1-mediated gene activation by PIAS1.";
 RL Proc. Natl. Acad. Sci. U.S.A. 95:10626-10631 (1998).

CC -!- FUNCTION: Specifically inhibits activated STAT1 signaling by
 CC blocking its DNA-binding activity.
 CC -!- SUBCELLULAR LOCATION: Nuclear (By similarity).
 CC -!- SIMILARITY: Contains 1 SAP domain.
 CC -!- SIMILARITY: Contains 1 MIZ-type zinc finger.

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DR EMBL; AF077950; AAC36701.1; -;
 DR MGD; MGI:1913125; Pias1.
 DR InterPro; IPR003034; SAP.
 DR InterPro; IPR004181; Znf_MIZ.
 DR Pfam; PF02037; SAP; 1.
 DR Pfam; PF02891; zf-MIZ; 1.
 DR SMART; SM00513; SAP; 1.
 DR PROSITE; PS50800; SAP; 1.
 KW Repeat; Zinc-finger; Nuclear protein.

FT DOMAIN 11 45
 FT ZN_FING 331 383 MIZ-TYPE.
 FT DOMAIN 56 64 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
 FT DOMAIN 368 380 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).